

SEQUENCE LISTING

(1) GENERAL INFORMATION:



APPLICANTS:

Metz, James G.
Lardizabal, Kathryn D.
Lassner, Michael

TITLE OF INVENTION:

Nucleic Acid Sequences Encoding
a Plant Cytoplasmic Protein Involved in
Fatty Acyl-COA Metabolism

(iii) NUMBER OF SEQUENCES: 39

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Calgene, Inc.

(B) STREET: 1920 Fifth Street

(C) CITY: Davis

(D) STATE: CA

(E) COUNTRY: USA

(F) ZIP: 95616

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB

(B) COMPUTER: Apple Macintosh

(C) OPERATING SYSTEM: Macintosh 7.0

(D) SOFTWARE: Microsoft Word 5.1a

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PCT/US94/13686

(B) FILING DATE: 30-NOV-94

(C) CLASSIFICATION:

(vii) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE:

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/265,047

(B) FILING DATE: 23-JUN-94

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/160,602

(B) FILING DATE: 30-NOV-93

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/066,299

(B) FILING DATE: 20-MAY-93

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PCT/US92/09863

(B) FILING DATE: 13-NOV-92

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 07/933,411

(B) FILING DATE: 21-AUG-92

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 07/796,256

(B) FILING DATE: 20-NOV-91

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Donna E. Scherer

(B) REGISTRATION NUMBER: 34,719

(A) NAME: Carl J. Schwedler

(B) REGISTRATION NUMBER: 36,924

(C) REFERENCE/DOCKET NUMBER: CGNE 101-2 US

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (916) 753-6313

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(2) INFORMATION FOR SEQ ID NO: : 1

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1786 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AAATCCTCCA CTCATACACT CCACTTCTCT CTCTCTCTCT CTCTCTCTGA AACAAATTTGA 60

GTAGCAAAC TAAAAGAAA ATG GAG GAA ATG GGA AGC ATT TTA GAG TTT CTT 112
Met Glu Glu Met Gly Ser Ile Leu Glu Phe Leu
1 5 10

GAT AAC AAA GCC ATT TTG GTC ACT GGT GCT ACT GGC TCC TTA GCA AAA 160
Asp Asn Lys Ala Ile Leu Val Thr Gly Ala Thr Gly Ser Leu Ala Lys
15 20 25

ATT TTT GTG GAG AAG GTA CTG AGG AGT CAA CCG AAT GTG AAG AAA CTC 208
Ile Phe Val Glu Lys Val Leu Arg Ser Gln Pro Asn Val Lys Lys Leu
30 35 40

TAT CTT CTT TTG AGA GCA ACC GAT GAC GAG ACA GCT GCT CTA CGC TTG 256
Tyr Leu Leu Leu Arg Ala Thr Asp Asp Glu Thr Ala Ala Leu Arg Leu
45 50 55

CAA AAT GAG GTT TTT GGA AAA GAG TTG TTC AAA GTT CTG AAA CAA AAT 304
Gln Asn Glu Val Phe Gly Lys Glu Leu Phe Lys Val Leu Lys Gln Asn
60 65 70 75

TTA GGT GCA AAT TTC TAT TCC TTT GTA TCA GAA AAA GTG ACT GTA GTA 352
Leu Gly Ala Asn Phe Tyr Ser Phe Val Ser Glu Lys Val Thr Val Val
80 85 90

CCC GGT GAT ATT ACT GGT GAA GAC TTG TGT CTC AAA GAC GTC AAT TTG 400
Pro Gly Asp Ile Thr Gly Glu Asp Leu Cys Leu Lys Asp Val Asn Leu
95 100 105

AAG GAA GAA ATG TGG AGG GAA ATC GAT GTT GTT GTC AAT CTA GCT GCT 448
Lys Glu Glu Met Trp Arg Glu Ile Asp Val Val Val Asn Leu Ala Ala
110 115 120

ACA Thr 125	ATC Ile	AAC Asn	TTC Phe	ATT Ile	GAA Glu 130	AGG Arg	TAC Tyr	GAC Asp	GTG Val	TCT Ser 135	CTG Leu	CTT Leu	ATC Ile	AAC Asn	ACA Thr	496
TAT Tyr 140	GGA Gly	GCC Ala	AAG Lys	TAT Tyr	GTT Val 145	TTG Leu	GAC Asp	TTC Phe	GCG Ala	AAG Lys 150	AAG Lys	TGC Cys	AAC Asn	AAA Lys	TTA Leu 155	544
AAG Lys	ATA Ile	TTT Phe	GTT Val	CAT His 160	GTA Val	TCT Ser	ACT Thr	GCT Ala	TAT Tyr 165	GTA Val	TCT Ser	GGA Gly	GAG Glu	AAA Lys 170	AAT Asn	592
GGG Gly	TTA Leu	ATA Ile	CTG Leu 175	GAG Glu	AAG Lys	CCT Pro	TAT Tyr	TAT Tyr 180	ATG Met	GGC Gly	GAG Glu	TCA Ser	CTT Leu 185	AAT Asn	GGA Gly	640
AGA Arg	TTA Leu	GGT Gly 190	CTG Leu	GAC Asp	ATT Ile	AAT Asn	GTA Val 195	GAG Glu	AAG Lys	AAA Lys	CTT Leu	GTG Val 200	GAG Glu	GCA Ala	AAA Lys	688
ATC Ile 205	AAT Asn	GAA Glu	CTT Leu	CAA Gln	GCA Ala 210	GCG Ala	GGG Gly	GCA Ala	ACG Thr	GAA Glu 215	AAG Lys	TCC Ser	ATT Ile	AAA Lys	TCG Ser	736
ACA Thr 220	ATG Met	AAG Lys	GAC Asp	ATG Met	GGC Gly 225	ATC Ile	GAG Glu	AGG Arg	GCA Ala	AGA Arg 230	CAC His	TGG Trp	GGA Gly	TGG Trp	CCA Pro 235	784
AAT Asn	GTG Val	TAT Tyr	GTA Val	TTC Phe 240	ACC Thr	AAG Lys	GCA Ala	TTA Leu	GGG Gly 245	GAG Glu	ATG Met	CTT Leu	TTG Leu	ATG Met 250	CAA Gln	832
TAC Tyr	AAA Lys	GGG Gly	GAC Asp 255	ATT Ile	CCG Pro	CTT Leu	ACT Thr	ATT Ile 260	ATT Ile	CGT Arg	CCC Pro	ACC Thr	ATC Ile 265	ATC Ile	ACC Thr	880
AGC Ser	ACT Thr	TTT Phe 270	AAA Lys	GAG Glu	CCC Pro	TTT Phe	CCT Pro 275	GGT Gly	TGG Trp	GTT Val	GAA Glu	GGT Gly 280	GTC Val	AGG Arg	ACC Thr	928
ATC Ile 285	GAT Asp	AAT Asn	GTA Val	CCT Pro	GTA Val 290	TAT Tyr	TAT Tyr	GGT Gly	AAA Lys	GGG Gly 295	AGA Arg	TTG Leu	AGG Arg	TGT Cys	ATG Met	976

CTT Leu 300	TGC Cys	GGA Gly	CCC Pro	AGC Ser	ACA Thr 305	ATA Ile	ATT Ile	GAC Asp	CTG Leu	ATA Ile 310	CCG Pro	GCA Ala	GAT Asp	ATG Met	GTC Val 315	1024
GTG Val	AAT Asn	GCA Ala	ACG Thr	ATA Ile 320	GTA Val	GCC Ala	ATG Met	GTG Val	GCG Ala 325	CAC His	GCA Ala	AAC Asn	CAA Gln	AGA Arg 330	TAC Tyr	1072
GTA Val	GAG Glu	CCG Pro	GTG Val 335	ACA Thr	TAC Tyr	CAT His	GTG Val	GGA Gly 340	TCT Ser	TCA Ser	GCG Ala	GCG Ala	AAT Asn 345	CCA Pro	ATG Met	1120
AAA Lys	CTG Leu	AGT Ser 350	GCA Ala	TTA Leu	CCA Pro	GAG Glu	ATG Met 355	GCA Ala	CAC His	CGT Arg	TAC Tyr	TTC Phe 360	ACC Thr	AAG Lys	AAT Asn	1168
CCA Pro 365	TGG Trp	ATC Ile	AAC Asn	CCG Pro	GAT Asp	CGC Arg 370	AAC Asn	CCA Pro	GTA Val	CAT His	GTG Val 375	GGT Gly	CGG Arg	GCT Ala	ATG Met	1216
GTC Val 380	TTC Phe	TCC Ser	TCC Ser	TTC Phe	TCC Ser 385	ACC Thr	TTC Phe	CAC His	CTT Leu	TAT Tyr 390	CTC Leu	ACC Thr	CTT Leu	AAT Asn	TTC Phe 395	1264
CTC Leu	CTT Leu	CCT Pro	TTG Leu	AAG Lys 400	GTA Val	CTG Leu	GAG Glu	ATA Ile	GCA Ala 405	AAT Asn	ACA Thr	ATA Ile	TTC Phe	TGC Cys 410	CAA Gln	1312
TGG Trp	TTC Phe	AAG Lys	GGT Gly 415	AAG Lys	TAC Tyr	ATG Met	GAT Asp	CTT Leu 420	AAA Lys	AGG Arg	AAG Lys	ACG Thr	AGG Arg 425	TTG Leu	TTG Leu	1360
TTG Leu	CGT Arg	TTA Leu 430	GTA Val	GAC Asp	ATT Ile	TAT Tyr	AAA Lys 435	CCC Pro	TAC Tyr	CTC Leu	TTC Phe	TTC Phe 440	CAA Gln	GGC Gly	ATC Ile	1408
TTT Phe	GAT Asp 445	GAC Asp	ATG Met	AAC Asn	ACT Thr	GAG Glu 450	AAG Lys	TTG Leu	CGG Arg	ATT Ile	GCT Ala 455	GCA Ala	AAA Lys	GAA Glu	AGC Ser	1456
ATA Ile 460	GTT Val	GAA Glu	GCT Ala	GAT Asp	ATG Met 465	TTT Phe	TAC Tyr	TTT Phe	GAT Asp	CCC Pro 470	AGG Arg	GCA Ala	ATT Ile	AAC Asn	TGG Trp 475	1504

GAA GAT TAC TTC TTG AAA ACT CAT TTC CCA GGN GTC GTA GAG CAC GTT 1552
 Glu Asp Tyr Phe Leu Lys Thr His Phe Pro Gly Val Val Glu His Val
 480 485 490

CTT AAC TAAAAGTTAC GGTACGAAAA TGAGAAGATT GGAATGCATG CACCGAAAGN 1608
 Leu Asn

NCAACATAAA AGACGTGGTT AAAGTCATGG TCAAAAAAGA AATAAAATGC AGTTAGGTTT 1668

GTGTTGCAGT TTTGATTCTT TGTATTGTTA CTTGTACTTT TGATCTTTTT CTTTTTTAAT 1728

GAAATTTCTC TCTTTGTTTT GTGAAAAAAA AAAAAAAAAA GAGCTCCTGC AGAAGCTT 1786

(2) INFORMATION FOR SEQ ID NO: 2 :

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1733 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2 :

GGAACTCCAT CCCTTCCTCC CTCACTCCTC TCTCTACA ATG AAG GCC AAA ACA ATC 56
 Met Lys Ala Lys Thr Ile
 1 5

ACA AAC CCG GAG ATC CAA GTC TCC ACG ACC ATG ACC ACC ACG ACC ACG 104
 Thr Asn Pro Glu Ile Gln Val Ser Thr Thr Met Thr Thr Thr Thr Thr
 10 15 20

ACT ATG ACC GCC ACT CTC CCC AAC TTC AAG TCC TCC ATC AAC TTA CAC 152
 Thr Met Thr Ala Thr Leu Pro Asn Phe Lys Ser Ser Ile Asn Leu His
 25 30 35

CAC GTC AAG CTC GGC TAC CAC TAC TTA ATC TCC AAT GCC CTC TTC CTC 200
 His Val Lys Leu Gly Tyr His Tyr Leu Ile Ser Asn Ala Leu Phe Leu
 40 45 50

GTA Val 55	TTC Phe	ATC Ile	CCC Pro	CTT Leu	TTG Leu 60	GGC Gly	CTC Leu	GCT Ala	TCG Ser	GCC Ala 65	CAT His	CTC Leu	TCC Ser	TCC Ser	TTC Phe 70	248
TCG Ser	GCC Ala	CAT His	GAC Asp	TTG Leu 75	TCC Ser	CTG Leu	CTC Leu	TTC Phe	GAC Asp 80	CTC Leu	CTT Leu	CGC Arg	CGC Arg	AAC Asn 85	CTC Leu	296
CTC Leu	CCT Pro	GTT Val	GTC Val 90	GTT Val	TGT Cys	TCT Ser	TTC Phe	CTC Leu 95	TTC Phe	GTT Val	TTA Leu	TTA Leu	GCA Ala 100	ACC Thr	CTA Leu	344
CAT His	TTC Phe	TTG Leu 105	ACC Thr	CGG Arg	CCC Pro	AGG Arg	AAT Asn 110	GTC Val	TAC Tyr	TTG Leu	GTG Val	GAC Asp 115	TTT Phe	GGA Gly	TGC Cys	392
TAT Tyr	AAG Lys 120	CCT Pro	CAA Gln	CCG Pro	AAC Asn	CTG Leu 125	ATG Met	ACA Thr	TCC Ser	CAC His	GAG Glu 130	ATG Met	TTC Phe	ATG Met	GAC Asp	440
CGG Arg 135	ACC Thr	TCC Ser	CGG Arg	GCC Ala	GGG Gly 140	TCG Ser	TTT Phe	TCT Ser	AAG Lys	GAG Glu 145	AAT Asn	ATT Ile	GAG Glu	TTT Phe	CAG Gln 150	488
AGG Arg	AAG Lys	ATC Ile	TTG Leu	GAG Glu 155	AGG Arg	GCC Ala	GGT Gly	ATG Met	GGT Gly 160	CGG Arg	GAA Glu	ACC Thr	TAT Tyr	GTC Val 165	CCC Pro	536
GAA Glu	TCC Ser	GTC Val	ACT Thr 170	AAG Lys	GTG Val	CCC Pro	GCC Ala	GAG Glu 175	CCG Pro	AGC Ser	ATA Ile	GCA Ala	GCA Ala 180	GCC Ala	AGG Arg	584
GCC Ala	GAG Glu	GCG Ala 185	GAG Glu	GAG Glu	GTG Val	ATG Met	TAC Tyr 190	GGG Gly	GCG Ala	ATC Ile	GAC Asp	GAG Glu 195	GTG Val	TTG Leu	GAG Glu	632
AAG Lys	ACG Thr 200	GGG Gly	GTG Val	AAG Lys	CCG Pro	AAG Lys 205	CAG Gln	ATA Ile	GGA Gly	ATA Ile	CTG Leu 210	GTG Val	GTG Val	ANC Xxx	TGC Cys	680
AGC Ser 215	TTG Leu	TTT Phe	AAC Asn	CCA Pro	ACG Thr 220	CCG Pro	TCG Ser	CTG Leu	TCA Ser	TCC Ser 225	ATG Met	ATA Ile	GTT Val	AAC Asn	CAT His 230	728

TAC Tyr	AAG Lys	CTN Leu	AGG Arg	GGT Gly 235	AAT Asn	ATA Ile	CTT Leu	AGC Ser	TAT Tyr 240	AAT Asn	CTT Leu	GGT Gly	GGC Gly	ATG Met 245	GGT Gly	776
TGC Cys	AGT Ser	GCT Ala	GGG Gly 250	CTC Leu	ATT Ile	TCC Ser	ATT Ile	GAT Asp 255	CTT Leu	GCC Ala	AAG Lys	GAC Asp	CTC Leu 260	CTA Leu	CAG Gln	824
GTT Val	TAC Tyr	CGT Arg 265	AAA Lys	AAC Asn	ACA Thr	TAT Tyr	GTG Val 270	TTA Leu	GTA Val	GTG Val	AGC Ser	ACG Thr 275	GAA Glu	AAC Asn	ATG Met	872
ACC Thr	CTT Leu 280	AAT Asn	TGG Trp	TAC Tyr	TGG Trp	GGC Gly 285	AAT Asn	GAC Asp	CGC Arg	TCC Ser	ATG Met 290	CTT Leu	ATC Ile	ACC Thr	AAC Asn	920
TGC Cys 295	CTA Leu	TTT Phe	CGC Arg	ATG Met	GGT Gly 300	GGC Gly	GCT Ala	GCC Ala	ATC Ile	ATC Ile 305	CTC Leu	TCA Ser	AAC Asn	CGC Arg	TGG Trp 310	968
CGT Arg	GAT Asp	CGT Arg	CGC Arg	CGA Arg 315	TCC Ser	AAG Lys	TAC Tyr	CAA Gln	CTC Leu 320	CTT Leu	CAT His	ACA Thr	GTA Val	CGC Arg 325	ACC Thr	1016
CAC His	AAG Lys	GGC Gly	GCT Ala 330	GAC Asp	GAC Asp	AAG Lys	TCC Ser	TAT Tyr 335	AGA Arg	TGC Cys	GTC Val	TTA Leu	CAA Gln 340	CAA Gln	GAA Glu	1064
GAT Asp	GAA Glu	AAT Asn 345	AAC Asn	AAG Lys	GTA Val	GGT Gly 350	GTT Val	GCC Ala	TTA Leu	TCC Ser	AAG Lys	GAT Asp 355	CTG Leu	ATG Met	GCA Ala	1112
GTT Val	GCC Ala 360	GGT Gly	GAA Glu	GCC Ala	CTA Leu	AAG Lys 365	GCC Ala	AAC Asn	ATC Ile	ACG Thr	ACC Thr 370	CTT Leu	GGT Gly	CCC Pro	CTC Leu	1160
GTG Val 375	CTC Leu	CCC Pro	ATG Met	TCA Ser	GAA Glu 380	CAA Gln	CTC Leu	CTC Leu	TTC Phe	TTT Phe 385	GCC Ala	ACC Thr	TTA Leu	GTG Val	GCA Ala 390	1208
CGT Arg	AAG Lys	GTC Val	TTC Phe	AAG Lys 395	ATG Met	ACG Thr	AAC Asn	GTG Val	AAG Lys 400	CCA Pro	TAC Tyr	ATC Ile	CCA Pro	GAT Asp 405	TTC Phe	1256

AAG	TTG	GCA	GCG	AAC	GAC	TTC	TGC	ATC	CAT	GCA	GGA	GGC	AAA	GCA	GTG	1304	
Lys	Leu	Ala	Ala	Asn	Asp	Phe	Cys	Ile	His	Ala	Gly	Gly	Lys	Ala	Val		
			410					415					420				
TTG	GAT	GAG	CTC	GAG	AAG	AAC	TTG	GAG	TTG	ACG	CCA	TGG	CAC	CTT	GAA	1352	
Leu	Asp	Glu	Leu	Glu	Lys	Asn	Leu	Glu	Leu	Thr	Pro	Trp	His	Leu	Glu		
		425					430					435					
CCC	TCG	AGG	ATG	ACA	CTG	TAT	AGG	TTT	GGG	AAC	ACA	TCG	AGT	AGC	TCA	1400	
Pro	Ser	Arg	Met	Thr	Leu	Tyr	Arg	Phe	Gly	Asn	Thr	Ser	Ser	Ser	Ser		
	440					445					450						
TTA	TGG	TAC	GAG	TTG	GCA	TAC	GCT	GAA	GCA	AAA	GGG	AGG	ATC	CGT	AAG	1448	
Leu	Trp	Tyr	Glu	Leu	Ala	Tyr	Ala	Glu	Ala	Lys	Gly	Arg	Ile	Arg	Lys		
455					460					465					470		
GGT	GAT	CGA	ACT	TGG	ATG	ATT	GGA	TTT	GGT	TCA	GGT	TTC	AAG	TGT	AAC	1496	
Gly	Asp	Arg	Thr	Trp	Met	Ile	Gly	Phe	Gly	Ser	Gly	Phe	Lys	Cys	Asn		
				475					480					485			
AGT	GTT	GTG	TGG	AGG	GCT	TTG	AGG	AGT	GTC	AAT	CCG	GCT	AGA	GAG	AAG	1544	
Ser	Val	Val	Trp	Arg	Ala	Leu	Arg	Ser	Val	Asn	Pro	Ala	Arg	Glu	Lys		
			490					495					500				
AAT	CCT	TGG	ATG	GAT	GAA	ATT	GAG	AAG	TTC	CCT	GTC	CAT	GTG	CCT	AAA	1592	
Asn	Pro	Trp	Met	Asp	Glu	Ile	Glu	Lys	Phe	Pro	Val	His	Val	Pro	Lys		
		505					510					515					
ATC	GCA	CCT	ATC	GCT	TCG	TAGAACTGCT	AGGATGTGAT	TAGTAATGAA								1640	
Ile	Ala	Pro	Ile	Ala	Ser												
		520															
AAATGTGTAT	TATGTTAGTG	ATGTAGAAAA	AGAACTTTA	GTTGATGGGT	GAGAACATGT											1700	
CTCATTGAGA	ATAACGTGTG	CATCGTTGTG	TTG													1733	

(2) INFORMATION FOR SEQ ID NO:3 :

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1783 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3 :

GTCGACACA	ATG	AAG	GCC	AAA	ACA	ATC	ACA	AAC	CCG	GAG	ATC	CAA	GTC	TCC	51	
	Met	Lys	Ala	Lys	Thr	Ile	Thr	Asn	Pro	Glu	Ile	Gln	Val	Ser		
	1				5					10						
ACG	ACC	ATG	ACC	ACC	ACG	ACC	ACG	ACC	GCC	ACT	CTC	CCC	AAC	TTC	AAG	99
Thr	Thr	Met	Thr	Thr	Thr	Thr	Thr	Thr	Ala	Thr	Leu	Pro	Asn	Phe	Lys	
15					20					25					30	
TCC	TCC	ATC	AAC	TTA	CAC	CAC	GTC	AAG	CTC	GGC	TAC	CAC	TAC	TTA	ATC	147
Ser	Ser	Ile	Asn	Leu	His	His	Val	Lys	Leu	Gly	Tyr	His	Tyr	Leu	Ile	
				35					40					45		
TCC	AAT	GCC	CTC	TTC	CTC	GTA	TTC	ATC	CCC	CTT	TTG	GGC	CTC	GCT	TCG	195
Ser	Asn	Ala	Leu	Phe	Leu	Val	Phe	Ile	Pro	Leu	Leu	Gly	Leu	Ala	Ser	
			50					55					60			
GCC	CAC	CTC	TCC	TCC	TTC	TCG	GCC	CAT	GAC	TTG	TCC	CTG	CTC	TTC	GAC	243
Ala	His	Leu	Ser	Ser	Phe	Ser	Ala	His	Asp	Leu	Ser	Leu	Leu	Phe	Asp	
		65					70					75				
CTC	CTT	CGC	CGC	AAC	CTC	CTC	CCC	GTT	GTC	GTT	TGT	TCT	TTC	CTC	TTC	291
Leu	Leu	Arg	Arg	Asn	Leu	Leu	Pro	Val	Val	Val	Cys	Ser	Phe	Leu	Phe	
	80					85					90					
GTT	TTA	TTA	GCA	ACC	CTA	CAT	TTC	TTG	ACC	CGG	CCT	AGG	AAT	GTC	TAC	339
Val	Leu	Leu	Ala	Thr	Leu	His	Phe	Leu	Thr	Arg	Pro	Arg	Asn	Val	Tyr	
95					100					105					110	
TTG	GTG	GAC	TTT	GCC	TGC	TAT	AAG	CCT	CAC	CCG	AAC	CTG	ATA	ACA	TCC	387
Leu	Val	Asp	Phe	Ala	Cys	Tyr	Lys	Pro	His	Pro	Asn	Leu	Ile	Thr	Ser	
				115					120					125		
CAC	GAG	ATG	TTC	ATG	GAC	CGG	ACC	TCC	CGG	GCC	GGG	TCG	TTT	TCT	AAG	435
His	Glu	Met	Phe	Met	Asp	Arg	Thr	Ser	Arg	Ala	Gly	Ser	Phe	Ser	Lys	
			130					135					140			
GAG	AAT	ATT	GAG	TTT	CAG	AGG	AAG	ATC	TTG	GAG	AGG	GCC	GGT	ATG	GGC	483
Glu	Asn	Ile	Glu	Phe	Gln	Arg	Lys	Ile	Leu	Glu	Arg	Ala	Gly	Met	Gly	
		145					150					155				

CGG Arg 160	GAA Glu 160	ACC Thr 160	TAC Tyr 160	GTC Val 160	CCC Pro 165	GAA Glu 165	TCC Ser 165	GTC Val 165	ACT Thr 165	AAG Lys 170	GTG Val 170	CCG Pro 170	CCC Pro 170	GAG Glu 170	CCG Pro 170	531
AGC Ser 175	ATA Ile 175	GCA Ala 175	GCA Ala 175	GCC Ala 175	AGG Arg 180	GCC Ala 180	GAG Glu 180	GCG Ala 180	GAG Glu 185	GAG Glu 185	GTG Val 185	ATG Met 185	TAC Tyr 185	GGG Gly 190	GCG Ala 190	579
ATC Ile 195	GAC Asp 195	GAG Glu 195	GTG Val 195	TTG Leu 195	GAG Glu 195	AAG Lys 195	ACG Thr 195	GGG Gly 200	GTG Val 200	AAG Lys 200	CCG Pro 200	AAG Lys 200	CAG Gln 205	ATA Ile 205	GGA Gly 205	627
ATA Ile 210	CTG Leu 210	GTG Val 210	GTG Val 210	AAC Asn 210	TGC Cys 210	AGC Ser 210	TTG Leu 215	TTT Phe 215	AAC Asn 215	CCA Pro 215	ACG Thr 215	CCG Pro 220	TCG Ser 220	CTG Leu 220	TCA Ser 220	675
TCC Ser 225	ATG Met 225	ATA Ile 225	GTT Val 225	AAC Asn 225	CAT His 225	TAC Tyr 230	AAG Lys 230	CTT Leu 230	AGG Arg 230	GGT Gly 230	AAT Asn 235	ATA Ile 235	CTT Leu 235	AGC Ser 235	TAT Tyr 235	723
AAT Asn 240	CTT Leu 240	GGT Gly 240	GGC Gly 240	ATG Met 240	GGT Gly 245	TGC Cys 245	AGT Ser 245	GCT Ala 245	GGG Gly 245	CTC Leu 250	ATT Ile 250	TCC Ser 250	ATT Ile 250	GAT Asp 250	CTT Leu 250	771
GCC Ala 255	AAG Lys 255	GAC Asp 255	CTC Leu 255	CTA Leu 255	CAG Gln 260	GTT Val 260	TAC Tyr 260	CGT Arg 260	AAC Asn 265	ACA Thr 265	TAT Tyr 265	GTG Val 265	TTA Leu 265	GTA Val 270	GTG Val 270	819
AGC Ser 275	ACA Thr 275	GAA Glu 275	AAC Asn 275	ATG Met 275	ACC Thr 275	CTT Leu 280	AAT Asn 280	TGG Trp 280	TAC Tyr 280	TGG Trp 280	GGC Gly 285	AAT Asn 285	GAC Asp 285	CGC Arg 285	TCC Ser 285	867
ATG Met 290	CTT Leu 290	ATC Ile 290	ACC Thr 290	AAC Asn 290	TGC Cys 295	CTA Leu 295	TTT Phe 295	CGC Arg 295	ATG Met 295	GGT Gly 300	GGC Gly 300	GCT Ala 300	GCC Ala 300	ATC Ile 300	ATC Ile 300	915
CTC Leu 305	TCA Ser 305	AAC Asn 305	CGC Arg 305	TGG Trp 310	CGT Arg 310	GAT Asp 310	CGT Arg 310	CGC Arg 310	CGA Arg 310	TCC Ser 315	AAG Lys 315	TAC Tyr 315	CAA Gln 315	CTC Leu 315	CTT Leu 315	963
CAC His 320	ACA Thr 320	GTA Val 320	CGC Arg 320	ACC Thr 320	CAC His 325	AAG Lys 325	GGC Gly 325	GCT Ala 325	GAC Asp 330	GAC Asp 330	AAG Lys 330	TCC Ser 330	TAT Tyr 330	AGA Arg 330	TGC Cys 330	1011

GTC Val 335	TTA Leu	CAA Gln	CAA Gln	GAA Glu	GAT Asp 340	GAA Glu	AAT Asn	AAC Asn	AAG Lys	GTA Val 345	GGT Gly	GTT Val	GCC Ala	TTA Leu	TCC Ser 350	1059
AAG Lys	GAT Asp	CTG Leu	ATG Met	GCA Ala 355	GTT Val	GCC Ala	GGT Gly	GAA Glu	GCC Ala 360	CTA Leu	AAG Lys	GCC Ala	AAC Asn	ATC Ile 365	ACG Thr	1107
ACC Thr	CTT Leu	GGT Gly	CCC Pro 370	CTC Leu	GTG Val	CTC Leu	CCC Pro	ATG Met 375	TCA Ser	GAA Glu	CAA Gln	CTC Leu	CTC Leu	TTC Phe 380	TTT Phe	1155
GCC Ala	ACC Thr	TTA Leu 385	GTG Val	GCA Ala	CGT Arg	AAG Lys	GTC Val 390	TTC Phe	AAG Lys	ATG Met	ACG Thr	AAC Asn 395	GTG Val	AAG Lys	CCA Pro	1203
TAC Tyr	ATC Ile 400	CCA Pro	GAT Asp	TTC Phe	AAG Lys	TTG Leu 405	GCA Ala	GCG Ala	AAG Lys	CAC His	TTC Phe 410	TGC Cys	ATC Ile	CAT His	GCA Ala	1251
GGA Gly 415	GGC Gly	AAA Lys	GCA Ala	GTG Val	TTG Leu 420	GAT Asp	GAG Glu	CTC Leu	GAG Glu	ACG Thr 425	AAC Asn	TTG Leu	GAG Glu	TTG Leu	ACG Thr 430	1299
CCA Pro	TGG Trp	CAC His	CTT Leu	GAA Glu 435	CCC Pro	TCG Ser	AGG Arg	ATG Met	ACA Thr 440	CTG Leu	TAT Tyr	AGG Arg	TTT Phe	GGG Gly 445	AAC Asn	1347
ACA Thr	TCG Ser	AGT Ser	AGC Ser 450	TCA Ser	TTA Leu	TGG Trp	TAC Tyr	GAG Glu 455	TTG Leu	GCA Ala	TAC Tyr	GCT Ala	GAA Glu 460	GCA Ala	AAA Lys	1395
GGG Gly	AGG Arg	ATC Ile 465	CGT Arg	AAG Lys	GGT Gly	GAT Asp	CGA Arg 470	ACT Thr	TGG Trp	ATG Met	ATT Ile	GGA Gly 475	TTT Phe	GGT Gly	TCA Ser	1443
GGT Gly	TTC Phe 480	AAG Lys	TGT Cys	AAC Asn	AGT Ser	GTT Val 485	GTG Val	TGG Trp	AGG Arg	GCT Ala	TTG Leu 490	AGG Arg	AGT Ser	GTC Val	AAT Asn	1491
CCG Pro 495	GCT Ala	AGA Arg	GAG Glu	AAG Lys	AAT Asn 500	CCT Pro	TGG Trp	ATG Met	GAT Asp	GAA Glu 505	ATT Ile	GAG Glu	AAT Asn	TTC Phe	CCT Pro 510	1539

GTC CAT GTG CCT AAA ATC GCA CCT ATC GCT TCG TAGAACTGCT AGGATGTGAT 1592
Val His Val Pro Lys Ile Ala Pro Ile Ala Ser
515 520

TATCGAAGGG	GAGGGAGAAA	GAGTGACGTG	GAGAAATAAG	AAACCGTTAA	GAGTCGGATA	600
TTTATCATAT	TAAAAGCCCA	ATGGGCCTGA	ACCCATTTAA	ACAAGACAGA	TAAATGGGCC	660
GTGTGTTAAG	TTAACAGAGT	GTTAACGTTT	GGTTTCAAAT	GCCAACGCCA	TAGGAACAAA	720
ACAAACGTGT	CCTCAAGTAA	ACCCCTGCCG	TTTACACCTC	AATGGCTGCA	TGGTGAAGCC	780
ATTAACACGT	GGCGTAGGAT	GCATGACGAC	GCCATTGACA	CCTGACTCTC	TTCCCTTCTC	840
TTCATATATC	TCTAATCAAT	TCAACTACTC	ATTGTCATAG	CTATTCGGAA	AATACATACA	900
CATCCTTTTC	TCTTCGATCT	CTCTCAATTC	ACAAGAAGCA	AAGTCGACGG	ATCCCTGCAG	960
TAAATTACGC	CATGACTATT	TTCATAGTCC	AATAAGGCTG	ATGTCGGGAG	TCCAGTTTAT	1020
GAGCAATAAG	GTGTTTAGAA	TTTGATCAAT	GTTTATAATA	AAAGGGGGAA	GATGATATCA	1080
CAGTCTTTTG	TTCTTTTTTG	CTTTTGTTAA	ATTTGTGTGT	TTCTATTTGT	AAACCTCCTG	1140
TATATGTTGT	ACTTCTTTCC	CTTTTAAAGT	GGTATCGTCT	ATATGGTAAA	ACGTTATGTT	1200
TGGTCTTTCC	TTTTCTCTGT	TTAGGATAAA	AAGACTGCAT	GTTTTATCTT	TAGTTATATT	1260
ATGTTGAGTA	AATGAACTTT	CATAGATCTG	GTTCCGTAGA	GTAGACTAGC	AGCCGAGCTG	1320
AGCTGAACTG	AACAGCTGGC	AATGTGAACA	CTGGATGCAA	GATCAGATGT	GAAGATCTCT	1380
AATATGGTGG	TGGGATTGAA	CATATCGTGT	CTATATTTTT	GTTGGCATT	AGCTCTTAAC	1440
ATAGATATAA	CTGATGCAGT	CATTGGTTCA	TACACATATA	TAGTAAGGAA	TTACAATGGC	1500
AACCCAAACT	TCAAAAACAG	TAGGCCACCT	GAATTGCCTT	ATCGAATAAG	AGTTTGTTTC	1560

CCCCCACTTC ATGGGATGTA ATACATGGGA TTTGGGAGTT TGAATGAACG TTGAGACATG 1620

GCAGAACCTC TAGAGGTACC GGCGCGC 1647

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 residues

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5 :

Glu Thr Tyr Val Pro Glu Ser Val Thr Lys Lys
 5 10

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 residues

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6 :

Val Pro Xaa Glu Pro Ser Ile Ala Ala Xaa
 5 10

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 residues

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7 :

Glu Thr Tyr Val Pro Glu Glu Val Thr Lys
5 10

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 residues

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8 :

Asp Leu Met Ala Val Ala Gly Glu Ala Leu Lys
5 10

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 residues

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9 :

Met Thr Asn Val Lys Pro Tyr Ile Pro Asp Phe
5 10

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 residues

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10 :

Phe Leu Pro Xaa Xaa Val Ala Ile Thr Gly Glu
 5 10

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 residues

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11 :

Phe Gly Asn Thr Ser Ser Xaa Xaa Leu Tyr Xaa Glu Leu Ala Tyr Ala
 5 10 15
Lys

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 residues

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12 :

Ala Glu Ala Glu Glu Val Met Tyr Gly Ala Ile Asp Glu Val Leu Glu
 5 10 15
Lys

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 residues

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13 :

Xaa Asp Ile Ala Ile Ile Gly Ser Gly Ser Ala Gly Leu Ala Gln Ala
 5 10 15
Xaa Ile Leu Lys Asp Ala Gly
 20

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 residues

(B) TYPE: amino acids

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14 :

Gln Gln Phe Thr Val Trp Xaa Asn Ala Ser Glu Pro Ser
 5 10

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other

(A) synthetic oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15 :

AAYATHACNA CNYTNGG

17

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other

- (A) synthetic oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16 :

SWRTTRCAYT TRAANCC

17

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1810 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17 :

GAA	ATG	AGT	AGG	TCT	AGC	GAA	CAA	GAT	CTA	CTC	TCT	ACC	GAG	ATT	GTT	48
Met	Ser	Arg	Ser	Ser	Glu	Gln	Asp	Leu	Leu	Ser	Thr	Glu	Ile	Val		
1				5				10						15		
AAC	CGT	GGG	ATC	GAA	CCT	TCC	GGT	CCA	AAC	GCC	GGT	TCA	CCA	ACG	TTC	96
Asn	Arg	Gly	Ile	Glu	Pro	Ser	Gly	Pro	Asn	Ala	Gly	Ser	Pro	Thr	Phe	
				20				25						30		
TCG	GTC	AGA	GTC	CGG	AGA	CGT	TTA	CCG	GAT	TTT	CTT	CAA	TCC	GTA	AAC	144
Ser	Val	Arg	Val	Arg	Arg	Arg	Leu	Pro	Asp	Phe	Leu	Gln	Ser	Val	Asn	
			35				40						45			

TTG Leu	AAG Lys	TAC Tyr 50	GTG Val	AAA Lys	CTT Leu	GGT Gly	TAT Tyr 55	CAC His	TAC Tyr	CTC Leu	ATA Ile	AAC Asn 60	CAT His	GCG Ala	GTT Val	192
TAC Tyr	TTG Leu 65	GCG Ala	ACG Thr	ATA Ile	CCG Pro	GTT Val 70	CTT Leu	GTG Val	CTT Leu	GTG Val	TTT Phe 75	AGT Ser	GCC Ala	GAA Glu	GTT Val	240
GGG Gly 80	AGT Ser	TTA Leu	AGC Ser	GGA Gly	GAA Glu 85	GAG Glu	ATT Ile	TGG Trp	AAG Lys	AAG Lys 90	CTT Leu	TGG Trp	GAC Asp	TAT Tyr	GAT Asp 95	288
ATC Ile	GCA Ala	ACC Thr	GTC Val	ATC Ile 100	GGA Gly	TTC Phe	TTC Phe	GGT Gly	GTC Val 105	TTT Phe	GTC Val	TTG Leu	ACC Thr	GTT Val 110	TGC Cys	336
GTC Val	TAC Tyr	TTC Phe	ATG Met 115	TCT Ser	CGT Arg	CCA Pro	CGA Arg	TCT Ser 120	GTT Val	TAT Tyr	CTC Leu	ATT Ile	GAC Asp 125	TTC Phe	GCT Ala	384
TGT Cys	TTC Phe	AAG Lys 130	CCT Pro	TCC Ser	GAT Asp	GAA Glu	CTT Leu 135	AAG Lys	GTG Val	ACA Thr	AGA Arg	GAA Glu 140	GAG Glu	TTC Phe	ATA Ile	432
GAT Asp	CTA Leu 145	GCT Ala	AGA Arg	AAA Lys	TCA Ser	GGC Gly 150	AAG Lys	TTC Phe	GAC Asp	GAA Glu	GAG Glu 155	ATC Ile	CTC Leu	GGA Gly	TTC Phe	480
AAG Lys 160	AAG Lys	AGG Arg	ATC Ile	CTT Leu	CAA Gln 165	GCC Ala	TCA Ser	GGA Gly	ATA Ile	GGC Gly 170	GAT Asp	GAA Glu	ACG Thr	TAC Tyr	GTC Val 175	528
CCA Pro	AGA Arg	TCA Ser	ATC Ile	TCT Ser 180	TCG Ser	TCG Ser	GAA Glu	AAC Asn	ACA Thr 185	ACA Thr	ACG Thr	ATG Met	AAA Lys	GAA Glu 190	GGT Gly	576
CGT Arg	GAA Glu	GAA Glu	GCC Ala 195	TCG Ser	ATG Met	ATG Met	ATA Ile	TTC Phe 200	GGC Gly	GCA Ala	CTC Leu	GAC Asp 205	GAA Glu 205	CTC Leu	TTC Phe	624
GAG Glu	AAG Lys	ACA Thr 210	CGT Arg	GTC Val	AAA Lys	CCG Pro	AAA Lys 215	GAC Asp	GTA Val	GGT Gly	GTC Val	CTC Leu 220	GTG Val	GTT Val	AAC Asn	672

TGC Cys 225	AGT Ser	ATC Ile	TTT Phe	AAC Asn	CCG Pro	ACT Thr 230	CCG Pro	TCA Ser	CTC Leu	TCC Ser	GCG Ala 235	ATG Met	GTG Val	ATT Ile	AAC Asn	720
CAC His 240	TAC Tyr	AAG Lys	ATG Met	AGA Arg	GGG Gly 245	AAC Asn	ATA Ile	CTT Leu	AGC Ser	TAC Tyr 250	AAC Asn	CTA Leu	GGA Gly	GGG Gly	ATG Met 255	768
GGT Gly	TGC Cys	TCA Ser	GCA Ala	GGA Gly 260	ATC Ile	ATA Ile	GCC Ala	GTT Val	GAT Asp 265	CTT Leu	GCT Ala	CGT Arg	GAC Asp	ATG Met 270	CTT Leu	816
CAG Gln	TCT Ser	AAC Asn	CCG Pro 275	AAT Asn	AGT Ser	TAC Tyr	GCG Ala	GTG Val 280	GTT Val	GTG Val	AGT Ser	ACC Thr	GAG Glu 285	ATG Met	GTT Val	864
GGG Gly	TAT Tyr	AAT Asn 290	TGG Trp	TAC Tyr	GTG Val	GGA Gly	CGT Arg 295	GAC Asp	AAG Lys	TCA Ser	ATG Met	GTT Val 300	ATA Ile	CCT Pro	AAC Asn	912
TGC Cys 305	TTC Phe	TTT Phe	AGG Arg	ATG Met	GGT Gly	TGC Cys 310	TCC Ser	GCC Ala	GTT Val	ATG Met	CTG Leu 315	TCT Ser	AAC Asn	CGC Arg	CGC Arg	960
CGT Arg 320	GAC Asp	TTC Phe	CGC Arg	CAT His	GCT Ala 325	AAG Lys	TAC Tyr	CGC Arg	CTT Leu	GAG Glu 330	CAC His	ATT Ile	GTC Val	CGG Arg	ACT Thr 335	1008
CAC His	AAG Lys	GCT Ala	GCC Ala	GAC Asp 340	GAC Asp	CGT Arg	AGC Ser	TTC Phe	AGG Arg 345	AGT Ser	GTG Val	TAC Tyr	CAG Gln	GAA Glu 350	GAA Glu	1056
GAT Asp	GAA Glu	CAA Gln	GGA Gly 355	TTC Phe	AAG Lys	GGA Gly	TTA Leu	AAA Lys 360	ATA Ile	AGC Ser	AGA Arg	GAC Asp	CTA Leu 365	ATG Met	GAA Glu	1104
GTT Val	GGA Gly 370	GGT Gly	GAA Glu	GCT Ala	CTC Leu	AAG Lys	ACC Thr 375	AAC Asn	ATC Ile	ACC Thr	ACC Thr	TTA Leu 380	GGC Gly	CCT Pro	CTC Leu	1152
GTC Val 385	CTT Leu	CCT Pro	TTC Phe	TCC Ser	GAG Glu	CAG Gln 390	CTT Leu	CTC Leu	TTC Phe	TTT Phe	GCC Ala 395	GCT Ala	TTG Leu	ATC Ile	CGT Arg	1200

AGA Arg 400	ACT Thr	TTC Phe	TCA Ser	CCC Pro	GCC Ala 405	GCC Ala	AAA Lys	ACT Thr	ACC Thr	ACC Thr 410	ACC Thr	TCC Ser	TCC Ser	TCA Ser	GCC Ala 415	1248
ACT Thr	GCG Ala	AAA Lys	ATC Ile	AAC Asn 420	GGA Gly	GCC Ala	AAG Lys	TCG Ser	TCA Ser 425	TCC Ser	TCC Ser	TCT Ser	GAT Asp	CTA Leu 430	TCC Ser	1296
AAG Lys	CCG Pro	TAC Tyr	ATC Ile 435	CCG Pro	GAC Asp	TAC Tyr	AAG Lys	CTT Leu 440	GCC Ala	TTC Phe	GAG Glu	CAT His	TTC Phe 445	TGC Cys	TTC Phe	1344
CAC His	GCG Ala	GCA Ala 450	AGC Ser	AAA Lys	GCG Ala	GTG Val 455	CTT Leu 455	GAG Glu	GAG Glu	CTT Leu	CAG Gln	AAG Lys 460	AAT Asn	CTA Leu	GGC Gly	1392
TTG Leu 465	AGT Ser	GAT Asp	GAG Glu	AAC Asn	ATG Met	GAG Glu 470	GCT Ala	TCT Ser	AAG Lys	ATG Met	ACT Thr 475	TTA Leu	CAC His	AGG Arg	TTT Phe	1440
GGA Gly 480	AAC Asn	ACT Thr	TCC Ser	AGC Ser	AGT Ser 485	GGA Gly	ATC Ile	TGG Trp	TAC Tyr	GAG Glu 490	CTT Leu	GCT Ala	TAC Tyr	ATG Met	GAG Glu 495	1488
GCC Ala	AAG Lys	GAG Glu	AGT Ser	GTT Val 500	CGT Arg	AGA Arg	GGC Gly	GAT Asp	AGG Arg 505	GTT Val	TGG Trp	CAG Gln	ATT Ile	GCT Ala 510	TTT Phe	1536
GGG Gly	TCA Ser	GGT Gly	TTT Phe 515	AAG Lys	TGT Cys	AAC Asn	AGT Ser	GTG Val 520	GTT Val	TGG Trp	AAG Lys	GCA Ala	ATG Met 525	AGG Arg	AAG Lys	1584
GTG Val	AAG Lys 530	AAG Lys	CCG Pro	GCA Ala	AGG Arg	AAC Asn	AAT Asn 535	CCT Pro	TGG Trp	GTT Val	GAT Asp	TGC Cys 540	ATT Ile	AAC Asn	CGT Arg	1632
TAC Tyr 545	CCT Pro	GTC Val	GCT Ala	CTC Leu	545	545	545	545	545	545	545	545	545	545	545	1687
ATCATCTATG	ATCTCTCTTC	CTTGTTGTTG	GATGATAGAC	GTTTGTTTGC	TGGTCATTTCG	1747										
TATCTTAAGA	CTTCTATAAG	AATGGATGGT	TCAAGTCCAA	AAAAAAAAAA	AAAAAAAAAA	1807										
AAA						1810										

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1442 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18 :

GTCGACAAA	ATG	ACG	TCC	ATT	AAC	GTA	AAG	CTC	CTT	TAC	CAT	TAC	GTC	ATA	51
	Met	Thr	Ser	Ile	Asn	Val	Lys	Leu	Leu	Tyr	His	Tyr	Val	Ile	
	1				5					10					
ACC AAC CTT TTC AAC CTT TGT TTC TTT CCA TTA ACG GCG ATC GTC GCC															99
Thr Asn Leu Phe Asn Leu Cys Phe Phe Pro Leu Thr Ala Ile Val Ala															
15					20					25				30	
GGA AAA GCC TAT CGG CTT ACC ATA GAC GAT CTT CAC CAC TTA TAC TAT															147
Gly Lys Ala Tyr Arg Leu Thr Ile Asp Asp Leu His His Leu Tyr Tyr															
				35					40					45	
TCC TAT CTC CAA CAC AAC CTC ATA ACC ATT GCT CCA CTC TTT GCC TTC															195
Ser Tyr Leu Gln His Asn Leu Ile Thr Ile Ala Pro Leu Phe Ala Phe															
				50					55					60	
ACC GTT TTC GGT TCG GTT CTC TAC ATC GCA ACC CGG CCC AAA CCG GTT															243
Thr Val Phe Gly Ser Val Leu Tyr Ile Ala Thr Arg Pro Lys Pro Val															
			65					70					75		
TAC CTC GTT GAG TAC TCA TGC TAC CTT CCA CCA ACG CAT TGT AGA TCA															291
Tyr Leu Val Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser															
			80					85					90		
AGT ATC TCC AAG GTC ATG GAT ATC TTT TAC CAA GTA AGA AAA GCT GAT															339
Ser Ile Ser Lys Val Met Asp Ile Phe Tyr Gln Val Arg Lys Ala Asp															
95					100					105				110	

CCT	TCT	CGG	AAC	GGC	ACG	TGC	GAT	GAC	TCG	TCC	TGG	CTT	GAC	TTC	TTG	387
Pro	Ser	Arg	Asn	Gly	Thr	Cys	Asp	Asp	Ser	Ser	Trp	Leu	Asp	Phe	Leu	
				115					120					125		
AGG	AAG	ATT	CAA	GAA	CGT	TCA	GGT	CTA	GGC	GAT	GAA	ACC	CAC	GGG	CCC	435
Arg	Lys	Ile	Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	His	Gly	Pro	
			130					135					140			
GAG	GGG	CTG	CTT	CAG	GTC	CCT	CCC	CGG	AAG	ACT	TTT	GCG	GCG	GCG	CGT	483
Glu	Gly	Leu	Leu	Gln	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ala	Arg	
		145					150					155				
GAA	GAG	ACG	GAG	CAA	GTT	ATC	ATT	GGT	GCG	CTA	GAA	AAT	CTA	TTC	AAG	531
Glu	Glu	Thr	Glu	Gln	Val	Ile	Ile	Gly	Ala	Leu	Glu	Asn	Leu	Phe	Lys	
	160					165					170					
AAC	ACC	AAT	GTT	AAC	CCT	AAA	GAT	ATA	GGT	ATA	CTT	GTG	GTG	AAC	TCA	579
Asn	Thr	Asn	Val	Asn	Pro	Lys	Asp	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	
175					180				185						190	
AGC	ATG	TTT	AAT	CCA	ACT	CCT	TCG	CTC	TCC	GCG	ATG	GTC	GTT	AAC	ACT	627
Ser	Met	Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Thr	
				195					200					205		
TTC	AAG	CTC	CGA	AGC	AAC	GTA	AGA	AGC	TTT	AAC	CTT	GGT	GGC	ATG	GGT	675
Phe	Lys	Leu	Arg	Ser	Asn	Val	Arg	Ser	Phe	Asn	Leu	Gly	Gly	Met	Gly	
			210					215					220			
TGT	AGT	GCC	GGC	GTT	ATA	GCC	ATT	GAT	CTA	GCA	AAG	GAC	TTG	TTG	CAT	723
Cys	Ser	Ala	Gly	Val	Ile	Ala	Ile	Asp	Leu	Ala	Lys	Asp	Leu	Leu	His	
		225					230					235				
GTC	CAT	AAA	AAT	ACG	TAT	GCT	CTT	GTG	GTG	AGC	ACA	GAG	AAC	ATC	ACT	771
Val	His	Lys	Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	
	240					245					250					
TAT	AAC	ATT	TAC	GCT	GGT	GAT	AAT	AGG	TCC	ATG	ATG	GTT	TCA	AAT	TGC	819
Tyr	Asn	Ile	Tyr	Ala	Gly	Asp	Asn	Arg	Ser	Met	Met	Val	Ser	Asn	Cys	
255					260				265						270	
TTG	TTC	CGT	GTT	GGT	GGG	GCC	GCT	ATT	TTG	CTC	TCC	AAC	AAG	CCT	AGA	867
Leu	Phe	Arg	Val	Gly	Gly	Ala	Ala	Ile	Leu	Leu	Ser	Asn	Lys	Pro	Arg	
				275					280					285		

GAT Asp	CGT Arg	AGA Arg	CGG Arg 290	TCC Ser	AAG Lys	TAC Tyr	GAG Glu	CTA Leu 295	GTT Val	CAC His	ACG Thr	GTT Val	CGA Arg 300	ACG Thr	CAT His	915
ACC Thr	GGA Gly	GCT Ala 305	GAC Asp	GAC Asp	AAG Lys	TCT Ser	TTT Phe 310	CGT Arg	TGC Cys	GTG Val	CAA Gln	CAA Gln 315	GGA Gly	GAC Asp	GTT Val	963
GAG Glu	AAC Asn 320	GGC Gly	AAA Lys	ACC Thr	GGA Gly	GTG Val 325	AGT Ser	TTG Leu	TCC Ser	AAG Lys	GAC Asp 330	ATA Ile	ACC Thr	GAT Asp	GTT Val	1011
GCT Ala 335	GGT Gly	CGA Arg	ACG Thr	GTT Val	AAG Lys 340	AAA Lys	AAC Asn	ATA Ile	GCA Ala	ACG Thr 345	CTG Leu	GGT Gly	CCG Pro	TTG Leu	ATT Ile 350	1059
CTT Leu	CCG Pro	TTA Leu	AGC Ser	GAG Glu 355	AAA Lys	CTT Leu	CTT Leu	TTT Phe 360	TTC Phe	GTT Val	ACC Thr	TTC Phe	ATG Met	GGC Gly 365	AAG Lys	1107
AAA Lys	CTT Leu	TTC Phe	AAA Lys 370	GAC Asp	AAA Lys	ATC Ile	AAA Lys	CAT His 375	TAT Tyr	TAC Tyr	GTC Val	CCG Pro	GAC Asp 380	TTC Phe	AAG Lys	1155
CTT Leu	GCT Ala	ATC Ile 385	GAC Asp	CAT His	TTT Phe	TGT Cys	ATA Ile 390	CAT His	GCC Ala	GGA Gly	GGC Gly	AAA Lys 395	GCC Ala	GTG Val	ATT Ile	1203
GAT Asp	GTG Val 400	CTA Leu	GAG Glu	AAG Lys	AAC Asn	CTA Leu 405	GGC Gly	CTA Leu	GCA Ala	CCG Pro	ATC Ile 410	GAT Asp	GTA Val	GAG Glu	GCA Ala	1251
TCA Ser 415	AGA Arg	TCA Ser	ACG Thr	TTA Leu	CAT His 420	AGA Arg	TTT Phe	GGA Gly	AAC Asn	ACT Thr 425	TCA Ser	TCT Ser	AGC Ser	TCA Ser	ATA Ile 430	1299
TGG Trp	TAT Tyr	GAG Glu	TTG Leu	GCA Ala 435	TAC Tyr	ATA Ile	GAA Glu	GCA Ala	AAA Lys 440	GGA Gly	AGG Arg	ATG Met	AAG Lys	AAA Lys 445	GGT Gly	1347
AAT Asn	AAA Lys	GTT Val	TGG Trp 450	CAG Gln	ATT Ile	GCT Ala	TTA Leu	GGG Gly 455	TCA Ser	GGC Gly	TTT Phe	AAG Lys	TGT Cys 460	AAC Asn	AGT Ser	1395

GCA	GTT	TGG	GTG	GCT	CTA	AAC	AAT	GTC	AAA	GCT	TCC	AAA	TAGGATCC	1442
Ala	Val	Trp	Val	Ala	Leu	Asn	Asn	Val	Lys	Ala	Ser	Lys		
		465					470					475		

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1442 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19 :

GTCGACAAA	ATG	ACG	TCC	ATT	AAC	GTA	AAG	CTC	CTT	TAC	CAT	TAC	GTC	ATA	51	
	Met	Thr	Ser	Ile	Asn	Val	Lys	Leu	Leu	Tyr	His	Tyr	Val	Ile		
	1				5					10						
ACC	AAC	CTT	TTC	AAC	CTT	TGC	TTC	TTT	CCG	TTA	ACG	GCG	ATC	GTC	GCC	99
Thr	Asn	Leu	Phe	Asn	Leu	Cys	Phe	Phe	Pro	Leu	Thr	Ala	Ile	Val	Ala	
15					20					25					30	
GGA	AAA	GCC	TAT	CGG	CTT	ACC	ATA	GAC	GAT	CTT	CAC	CAC	TTA	TAC	TAT	147
Gly	Lys	Ala	Tyr	Arg	Leu	Thr	Ile	Asp	Asp	Leu	His	His	Leu	Tyr	Tyr	
				35					40					45		
TCC	TAT	CTC	CAA	CAC	AAC	CTC	ATA	ACC	ATC	GCT	CCA	CTC	TTT	GCC	TTC	195
Ser	Tyr	Leu	Gln	His	Asn	Leu	Ile	Thr	Ile	Ala	Pro	Leu	Phe	Ala	Phe	
			50					55					60			
ACC	GTT	TTC	GGT	TCG	GTT	CTC	TAC	ATC	GCA	ACC	CGG	CCC	AAA	CCG	GTT	243
Thr	Val	Phe	Gly	Ser	Val	Leu	Tyr	Ile	Ala	Thr	Arg	Pro	Lys	Pro	Val	
		65					70					75				
TAC	CTC	GTT	GAG	TAC	TCA	TGC	TAC	CTT	CCA	CCA	ACG	CAT	TGT	AGA	TCA	291
Tyr	Leu	Val	Glu	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Thr	His	Cys	Arg	Ser	
	80					85					90					

AGT Ser 95	ATC Ile	TCC Ser	AAG Lys	GTC Val	ATG Met 100	GAT Asp	ATC Ile	TTT Phe	TAT Tyr	CAA Gln 105	GTA Val	AGA Arg	AAA Lys	GCT Ala	GAT Asp 110	339
CCT Pro	TCT Ser	CGG Arg	AAC Asn	GGC Gly 115	ACG Thr	TGC Cys	GAT Asp	GAC Asp	TCG Ser 120	TCG Ser	TGG Trp	CTT Leu	GAC Asp	TTC Phe 125	TTG Leu	387
AGG Arg	AAG Lys	ATT Ile	CAA Gln 130	GAA Glu	CGT Arg	TCA Ser	GGT Gly	CTA Leu 135	GGC Gly	GAT Asp	GAA Glu	ACT Thr	CAC His 140	GGG Gly	CCC Pro	435
GAG Glu	GGG Gly	CTG Leu 145	CTT Leu	CAG Gln	GTC Val	CCT Pro	CCC Pro 150	CGG Arg	AAG Lys	ACT Thr	TTT Phe	GCG Ala 155	GCG Ala	GCG Ala	CGT Arg	483
GAA Glu 160	GAG Glu	ACG Thr	GAG Glu	CAA Gln	GTT Val	ATC Ile 165	ATT Ile	GGT Gly	GCG Ala	CTA Leu	GAA Glu 170	AAT Asn	CTA Leu	TTC Phe	AAG Lys	531
AAC Asn 175	ACC Thr	AAC Asn	GTT Val	AAC Asn	CCT Pro 180	AAA Lys	GAT Asp	ATA Ile	GGT Gly	ATA Ile 185	CTT Leu	GTG Val	GTG Val	AAC Asn	TCA Ser 190	579
AGC Ser	ATG Met	TTT Phe	AAT Asn	CCA Pro 195	ACT Thr	CCA Pro	TCG Ser	CTC Leu	TCC Ser 200	GCG Ala	ATG Met	GTC Val	GTT Val	AAC Asn 205	ACT Thr	627
TTC Phe	AAG Lys	CTC Leu	CGA Arg 210	AGC Ser	AAC Asn	GTA Val	AGA Arg	AGC Ser 215	TTT Phe	AAC Asn	CTT Leu	GGT Gly	GGC Gly 220	ATG Met	GGT Gly	675
TGT Cys	AGT Ser	GCC Ala 225	GGC Gly	GTT Val	ATA Ile	GCC Ala	ATT Ile 230	GAT Asp	CTA Leu	GCA Ala	AAG Lys	GAC Asp 235	TTG Leu	TTG Leu	CAT His	723
GTC Val 240	CAT His	AAA Lys	AAT Asn	ACG Thr	TAT Tyr	GCT Ala 245	CTT Leu	GTG Val	GTG Val	AGC Ser	ACA Thr 250	GAG Glu	AAC Asn	ATC Ile	ACT Thr	771
TAT Tyr 255	AAC Asn	ATT Ile	TAC Tyr	GCT Ala	GGT Gly 260	GAT Asp	AAT Asn	AGG Arg	TCC Ser	ATG Met 265	ATG Met	GTT Val	TCA Ser	AAT Asn	TGC Cys 270	819

TTG	TTC	CGT	GTT	GGT	GGG	GCC	GCT	ATT	TTG	CTC	TCC	AAC	AAG	CCT	GGA	867
Leu	Phe	Arg	Val	Gly	Gly	Ala	Ala	Ile	Leu	Leu	Ser	Asn	Lys	Pro	Gly	
				275					280					285		
GAT	CGT	AGA	CGG	TCC	AAG	TAC	GAG	CTA	GTT	CAC	ACG	GTT	CGA	ACG	CAT	915
Asp	Arg	Arg	Arg	Ser	Lys	Tyr	Glu	Leu	Val	His	Thr	Val	Arg	Thr	His	
			290					295					300			
ACC	GGA	GCT	GAC	GAC	AAG	TCT	TTT	CGT	TGC	GTG	CAA	CAA	GGA	GAC	GAT	963
Thr	Gly	Ala	Asp	Asp	Lys	Ser	Phe	Arg	Cys	Val	Gln	Gln	Gly	Asp	Asp	
		305					310					315				
GAG	AAC	GGC	AAA	ATC	GGA	GTG	AGT	TTG	TCC	AAG	GAC	ATA	ACC	GAT	GTT	1011
Glu	Asn	Gly	Lys	Ile	Gly	Val	Ser	Leu	Ser	Lys	Asp	Ile	Thr	Asp	Val	
	320					325					330					
GCT	GGT	CGA	ACG	GTT	AAG	AAA	AAC	ATA	GCA	ACG	TTG	GGT	CCG	TTG	ATT	1059
Ala	Gly	Arg	Thr	Val	Lys	Lys	Asn	Ile	Ala	Thr	Leu	Gly	Pro	Leu	Ile	
335					340					345					350	
CTT	CCG	TTA	AGC	GAG	AAA	CTT	CTT	TTT	TTC	GTT	ACC	TTC	ATG	GGC	AAG	1107
Leu	Pro	Leu	Ser	Glu	Lys	Leu	Leu	Phe	Phe	Val	Thr	Phe	Met	Gly	Lys	
				355					360					365		
AAA	CTT	TTC	AAA	GAT	AAA	ATC	AAA	CAT	TAC	TAC	GTC	CCG	GAT	TTC	AAA	1155
Lys	Leu	Phe	Lys	Asp	Lys	Ile	Lys	His	Tyr	Tyr	Val	Pro	Asp	Phe	Lys	
			370					375					380			
CTT	GCT	ATT	GAC	CAT	TTT	TGT	ATA	CAT	GCC	GGA	GGC	AGA	GCC	GTG	ATT	1203
Leu	Ala	Ile	Asp	His	Phe	Cys	Ile	His	Ala	Gly	Gly	Arg	Ala	Val	Ile	
		385					390					395				
GAT	GTG	CTA	GAG	AAG	AAC	CTA	GCC	CTA	GCA	CCG	ATC	GAT	GTA	GAG	GCA	1251
Asp	Val	Leu	Glu	Lys	Asn	Leu	Ala	Leu	Ala	Pro	Ile	Asp	Val	Glu	Ala	
	400					405					410					
TCA	AGA	TCA	ACG	TTA	CAT	AGA	TTT	GGA	AAC	ACT	TCA	TCT	AGC	TCA	ATA	1299
Ser	Arg	Ser	Thr	Leu	His	Arg	Phe	Gly	Asn	Thr	Ser	Ser	Ser	Ser	Ile	
415					420					425					430	
TGG	TAT	GAG	TTG	GCA	TAC	ATA	GAA	GCA	AAA	GGA	AGG	ATG	AAG	AAA	GGT	1347
Trp	Tyr	Glu	Leu	Ala	Tyr	Ile	Glu	Ala	Lys	Gly	Arg	Met	Lys	Lys	Gly	
				435					440					445		

AAT	AAA	GTT	TGG	CAG	ATT	GCT	TTA	GGG	TCA	GGC	TTT	AAG	TGT	AAC	AGT	1395
Asn	Lys	Val	Trp	Gln	Ile	Ala	Leu	Gly	Ser	Gly	Phe	Lys	Cys	Asn	Ser	
		450						455					460			

GCA	GTT	TGG	GTG	GCT	CTA	AAC	AAT	GTC	AAA	GCT	TCC	AAA	TAGGATCC	1442
Ala	Val	Trp	Val	Ala	Leu	Asn	Asn	Val	Lys	Ala	Ser	Lys		
		465					470					475		

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 623 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20 :

AAG	CTT	AAA	CTA	GTG	TAT	CAT	TAC	CTA	ATC	TCC	AAC	GCT	CTC	TAC	ATC	48
Lys	Leu	Lys	Leu	Val	Tyr	His	Tyr	Leu	Ile	Ser	Asn	Ala	Leu	Tyr	Ile	
1				5					10					15		

CTC	CTC	CTT	CCT	CTC	CTC	GCC	GCA	ACA	ATC	GCT	AAC	CTC	TCT	TCT	TTC	96
Leu	Leu	Leu	Pro	Leu	Leu	Ala	Ala	Thr	Ile	Ala	Asn	Leu	Ser	Ser	Phe	
			20					25					30			

ACC	ATC	AAC	GAC	CTC	TCT	CTC	CTC	TAC	AAC	ACA	CTC	CGT	TTC	CAT	TTC	144
Thr	Ile	Asn	Asp	Leu	Ser	Leu	Leu	Tyr	Asn	Thr	Leu	Arg	Phe	His	Phe	
		35					40					45				

CTC	TCC	GCC	ACA	CTC	GCC	ACC	GCA	CTC	TTG	ATC	TCT	CTC	TCC	ACC	GCT	192
Leu	Ser	Ala	Thr	Leu	Ala	Thr	Ala	Leu	Leu	Ile	Ser	Leu	Ser	Thr	Ala	
	50					55					60					

TAC	TTC	ACC	ACC	CGT	CCT	CGC	CGT	GTC	TTC	CTC	CTC	GAC	TTC	TCG	TGT	240
Tyr	Phe	Thr	Thr	Arg	Pro	Arg	Arg	Val	Phe	Leu	Leu	Asp	Phe	Ser	Cys	
65					70					75					80	

TAC	AAA	CCA	GAC	CCT	TCA	CTG	ATC	TGC	ACT	CGT	GAA	ACA	TTC	ATG	GAC	288
Tyr	Lys	Pro	Asp	Pro	Ser	Leu	Ile	Cys	Thr	Arg	Glu	Thr	Phe	Met	Asp	
				85					90					95		
AGA	TCT	CAA	CGT	GTA	GGC	ATC	TTC	ACA	GAA	GAC	AAC	TTA	GCT	TTC	CAA	336
Arg	Ser	Gln	Arg	Val	Gly	Ile	Phe	Thr	Glu	Asp	Asn	Leu	Ala	Phe	Gln	
			100					105					110			
CAA	AAG	ATC	CTC	GAA	AGA	TCC	GGT	CTA	GGT	CAG	AAA	ACT	TAC	TTC	CCT	384
Gln	Lys	Ile	Leu	Glu	Arg	Ser	Gly	Leu	Gly	Gln	Lys	Thr	Tyr	Phe	Pro	
		115					120					125				
GAA	GCT	CTT	CTT	CGT	GTT	CCT	CCT	AAT	CCT	TGT	ATG	GAA	GAA	GCG	AGA	432
Glu	Ala	Leu	Leu	Arg	Val	Pro	Pro	Asn	Pro	Cys	Met	Glu	Glu	Ala	Arg	
	130					135					140					
AAA	GAG	GCA	GAA	ACA	GTT	ATG	TTC	GGA	GCT	ATT	GAC	GCG	GTT	CTT	GAG	480
Lys	Glu	Ala	Glu	Thr	Val	Met	Phe	Gly	Ala	Ile	Asp	Ala	Val	Leu	Glu	
145					150					155					160	
AAG	ACC	GGT	GTG	AAA	CCT	AAA	GAT	ATT	GGA	ATC	CTT	GTG	GTG	AAT	TGT	528
Lys	Thr	Gly	Val	Lys	Pro	Lys	Asp	Ile	Gly	Ile	Leu	Val	Val	Asn	Cys	
				165					170					175		
AGC	TTG	TTT	AAT	CCA	ACA	CCG	TCA	CTT	TCT	GCT	ATG	ATT	GTG	AAT	AAG	576
Ser	Leu	Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Ile	Val	Asn	Lys	
			180					185					190			
TAT	AAG	CTT	AGA	GGC	AAC	ATT	TTG	AGC	TAT	AAT	TTC	GGC	GGG	ATG	GG	623
Tyr	Lys	Leu	Arg	Gly	Asn	Ile	Leu	Ser	Tyr	Asn	Phe	Gly	Gly	Met	Gly	
		195					200					205				

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 607 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cdna to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21 :

AAG Lys 1	CTT Leu	AAG Lys	TTA Leu	GGC Gly 5	TAC Tyr	CAC His	TAT Tyr	CTG Leu	ATC Ile 10	ACT Thr	CAC His	TTT Phe	TTT Phe	AAA Lys 15	CTC Leu	48
ATG Met	TTC Phe	CTC Leu	CCT Pro 20	CTA Leu	ATG Met	GCT Ala	GTT Val	TTG Leu 25	TTC Phe	ATG Met	AAT Asn	GTC Val	TCA Ser 30	TTG Leu	TTA Leu	96
AGC Ser	CTA Leu	AAC Asn 35	CAT His	CTT Leu	CAG Gln	CTC Leu	TAT Tyr 40	TAC Tyr	AAT Asn	TCC Ser	ACC Thr	GGA Gly 45	TTC Phe	ATC Ile	TTC Phe	144
GTC Val 50	ATC Ile	ACT Thr	CTC Leu	GCC Ala	ATT Ile	GTC Val 55	GGA Gly	TCC Ser	ATT Ile	GTC Val	TTC Phe 60	TTC Phe	ATG Met	TCT Ser	CGA Arg	192
CCT Pro 65	AGA Arg	TCC Ser	ATC Ile	TAC Tyr	CTT Leu 70	CTA Leu	GAT Asp	TAC Tyr	TCT Ser	TGC Cys 75	TAC Tyr	CTC Leu	CCG Pro	CCT Pro	TCG Ser 80	240
AGT Ser	CAA Gln	AAA Lys	GTT Val	AGC Ser 85	TAC Tyr	CAG Gln	AAA Lys	TTC Phe	ATG Met 90	AAC Asn	AAC Asn	TCT Ser	AGT Ser	TTG Leu 95	ATT Ile	288
CAA Gln	GAT Asp	TTC Phe	AGC Ser 100	GAA Glu	ACT Thr	TCT Ser	CTT Leu	GAG Glu 105	TTC Phe	CAG Gln	AGG Arg	AAG Lys	ATC Ile 110	TTG Leu	ATT Ile	336
CGC Arg	TCT Ser	GGT Gly 115	CTC Leu	GGT Gly	GAA Glu	GAG Glu	ACT Thr 120	TAT Tyr	TTA Leu	CCG Pro	GAT Asp	TCT Ser 125	ATT Ile	CAC His	TCT Ser	384
ATC Ile 130	CCT Pro	CCG Pro	CGT Arg	CCT Pro	ACT Thr	ATG Met 135	GCT Ala	GCA Ala	GCG Ala	CGT Arg	GAA Glu 140	GAA Glu	GCG Ala	GAG Glu	CAG Gln	432
GTA Val 145	ATC Ile	TTC Phe	GGT Gly	GCA Ala	CTC Leu 150	GAC Asp	AAT Asn	CTT Leu	TTC Phe	GAG Glu 155	AAT Asn	ACA Thr	AAA Lys	ATC Ile	AAT Asn 160	480

CCT	AGG	GAG	ATT	GGT	GTT	CTT	GTT	GTG	AAT	TGT	AGT	TTG	TTT	AAC	CCC	528
Pro	Arg	Glu	Ile	Gly	Val	Leu	Val	Val	Asn	Cys	Ser	Leu	Phe	Asn	Pro	
				165					170					175		
ACG	CCT	TCT	TTA	TCC	GCC	ATG	ATT	GTT	AAC	AAG	TAT	AAG	CTT	AGA	GGA	576
Thr	Pro	Ser	Leu	Ser	Ala	Met	Ile	Val	Asn	Lys	Tyr	Lys	Leu	Arg	Gly	
			180					185					190			
AAC	ATT	AAG	AGC	TTT	AAT	CTC	GGC	GGC	ATG	G						607
Asn	Ile	Lys	Ser	Phe	Asn	Leu	Gly	Gly	Met							
		195					200									

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 622 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

AAG	CTT	AAA	CTG	GGG	TAC	CAC	TAC	CTC	ATT	ACT	CAT	CTC	TTC	AAG	CTC	48
Lys	Leu	Lys	Leu	Gly	Tyr	His	Tyr	Leu	Ile	Thr	His	Leu	Phe	Lys	Leu	
1				5				10						15		
TGT	TTG	GTT	CCA	TTA	ATG	GCG	GTT	TTA	GTC	ACA	GAG	ATC	TCC	CGA	TTA	96
Cys	Leu	Val	Pro	Leu	Met	Ala	Val	Leu	Val	Thr	Glu	Ile	Ser	Arg	Leu	
			20					25					30			
ACA	ACA	GAC	GAT	CTT	TAC	CAG	ATT	TGC	CTT	CAT	CTC	CAA	TAC	AAT	CTC	144
Thr	Thr	Asp	Asp	Leu	Tyr	Gln	Ile	Cys	Leu	His	Leu	Gln	Tyr	Asn	Leu	
		35					40					45				
GTT	GCT	TTC	ATC	TTT	CTC	TCT	GCT	TTA	GCT	ATC	TTT	GGC	TCC	ACC	GTT	192
Val	Ala	Phe	Ile	Phe	Leu	Ser	Ala	Leu	Ala	Ile	Phe	Gly	Ser	Thr	Val	
	50					55					60					

TAC	ATC	ATG	AGT	CGT	CCC	AGA	TCT	GTT	TAT	CTC	GTT	GAT	TAC	TCT	TGT	240
Tyr	Ile	Met	Ser	Arg	Pro	Arg	Ser	Val	Tyr	Leu	Val	Asp	Tyr	Ser	Cys	
65					70					75					80	
TAT	CTT	CCT	CCG	GAG	AGT	CTT	CAG	GTT	AAG	TAT	CAG	AAG	TTT	ATG	GAT	288
Tyr	Leu	Pro	Pro	Glu	Ser	Leu	Gln	Val	Lys	Tyr	Gln	Lys	Phe	Met	Asp	
				85					90					95		
CAT	TCT	AAG	TTG	ATT	GAA	GAT	TTC	AAT	GAG	TCA	TCT	TTA	GAG	TTT	CAG	336
His	Ser	Lys	Leu	Ile	Glu	Asp	Phe	Asn	Glu	Ser	Ser	Leu	Glu	Phe	Gln	
			100					105					110			
AGG	AAG	ATT	CTT	GAA	CGT	TCT	GGT	TTA	GGA	GAA	GAG	ACT	TAT	CTC	CCT	384
Arg	Lys	Ile	Leu	Glu	Arg	Ser	Gly	Leu	Gly	Glu	Glu	Thr	Tyr	Leu	Pro	
		115					120					125				
GAA	GCT	TTA	CAT	TGT	ATC	CCT	CCG	AGG	CCT	ACG	ATG	ATG	GCG	GCT	CGT	432
Glu	Ala	Leu	His	Cys	Ile	Pro	Pro	Arg	Pro	Thr	Met	Met	Ala	Ala	Arg	
	130					135					140					
GAG	GAA	GCT	GAG	CAG	GTA	ATG	TTT	GGT	GCT	CTT	GAT	AAG	CTT	TTC	GAG	480
Glu	Glu	Ala	Glu	Gln	Val	Met	Phe	Gly	Ala	Leu	Asp	Lys	Leu	Phe	Glu	
145					150					155					160	
AAT	ACC	AAG	ATT	AAC	CCT	AGG	GAT	ATT	GGT	GTG	TTG	GTT	GTG	AAT	TGT	528
Asn	Thr	Lys	Ile	Asn	Pro	Arg	Asp	Ile	Gly	Val	Leu	Val	Val	Asn	Cys	
				165					170					175		
AGC	TTG	TTT	AAT	CCT	ACA	CCT	TCG	TTG	TCA	GCT	ATG	ATT	GTT	AAC	AAG	576
Ser	Leu	Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Ile	Val	Asn	Lys	
			180					185					190			
TAT	AAG	CTT	AGA	GGG	AAT	GTT	AAG	AGT	TTT	AAC	CTG	GGG	GGC	ATT	G	622
Tyr	Lys	Leu	Arg	Gly	Asn	Val	Lys	Ser	Phe	Asn	Leu	Gly	Gly	Ile		
		195					200					205				

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 625 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23 :

AAG CTT AAG TTA TGG TAT CAC TAC CTG ATT TCT CAC CTT TTT AAG CTC	48
Lys Leu Lys Leu Trp Tyr His Tyr Leu Ile Ser His Leu Phe Lys Leu	
1 5 10 15	
TTG TTG GTT CCT TTA ATG GCG GTT CTG TTC ACG AAT GTC TCC CGG TTA	96
Leu Leu Val Pro Leu Met Ala Val Leu Phe Thr Asn Val Ser Arg Leu	
20 25 30	
AGC CTA AAC CAG CTC TGT CTC GAT CTC TCT CTC CAG CTC CAG TTC AAT	144
Ser Leu Asn Gln Leu Cys Leu Asp Leu Ser Leu Gln Leu Gln Phe Asn	
35 40 45	
CTC GTC GGA TTC ATC TTC TTC ATT ACC GTC TCC ATT TTC GGA TTC ACA	192
Leu Val Gly Phe Ile Phe Phe Ile Thr Val Ser Ile Phe Gly Phe Thr	
50 55 60	
GTT ATC TTC ATG TCC CGA CCT AGA TCC GTT TAC CTC CTC GAC TAC TCA	240
Val Ile Phe Met Ser Arg Pro Arg Ser Val Tyr Leu Leu Asp Tyr Ser	
65 70 75 80	
TGT TAC CTC CCG CCG TCG AAT CTC AAA GTT AGC TAC CAG ACA TTC ATG	288
Cys Tyr Leu Pro Pro Ser Asn Leu Lys Val Ser Tyr Gln Thr Phe Met	
85 90 95	
AAT CAT TCT AAA CTG ATT GAA GAT TTC GAC GAG TCG TCG CTT GAG TTC	336
Asn His Ser Lys Leu Ile Glu Asp Phe Asp Glu Ser Ser Leu Glu Phe	
100 105 110	
CAG CGG AAG ATC CTG AAG CGA TCC GGT CTC GGC GAA GAG ACT TAC CTC	384
Gln Arg Lys Ile Leu Lys Arg Ser Gly Leu Gly Glu Glu Thr Tyr Leu	
115 120 125	
CCG GAA TCT ATC CAC TGC ATC CCG CCG CGT CCG ACT ATG GCG GCG GCG	432
Pro Glu Ser Ile His Cys Ile Pro Pro Arg Pro Thr Met Ala Ala Ala	
130 135 140	
CGT GAG GAA TCG GAG CAG GTA ATC TTC GGT GCA CTC GAC AAT CTC TTC	480
Arg Glu Glu Ser Glu Gln Val Ile Phe Gly Ala Leu Asp Asn Leu Phe	
145 150 155 160	

GAG	AAT	ACC	AAA	ATC	GAC	CCT	AGG	GAG	ATT	GGT	GTT	GTG	GTG	GTG	AAC	528
Glu	Asn	Thr	Lys	Ile	Asp	Pro	Arg	Glu	Ile	Gly	Val	Val	Val	Val	Asn	
				165					170						175	

TGC	AGC	TTG	TTT	AAC	CCG	ACG	CCT	TCT	TTA	TCC	GCC	ATG	ATT	GTG	AAC	576
Cys	Ser	Leu	Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Ile	Val	Asn	
			180					185						190		

AAG	TAT	AAG	CTT	AGA	GGA	AAC	GTG	AAG	AGC	TTT	AAT	CTC	GGT	GGC	ATG	G	625
Lys	Tyr	Lys	Leu	Arg	Gly	Asn	Val	Lys	Ser	Phe	Asn	Leu	Gly	Gly	Met		
		195					200					205					

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1704 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

GTTCATTGAT	TTGTTTGAGA	CTCTGTTGCA	GAAATCTCCA	C	ATG	GAT	GAT	GAA	TCC	56
					Met	Asp	Asp	Glu	Ser	
					1				5	

GTT	AAT	GGA	GGA	TCC	GTA	CAG	ATC	CGG	ACC	CGA	AAG	TAC	GTC	AAG	CTG	104
Val	Asn	Gly	Gly	Ser	Val	Gln	Ile	Arg	Thr	Arg	Lys	Tyr	Val	Lys	Leu	
				10				15						20		

GGT	TAT	CAC	TAC	CTG	ATT	TCT	CAC	CTT	TTT	AAG	CTC	TTG	TTG	GTT	CCT	152
Gly	Tyr	His	Tyr	Leu	Ile	Ser	His	Leu	Phe	Lys	Leu	Leu	Leu	Val	Pro	
			25					30					35			

TTA	ATG	GCG	GTT	CTG	TTC	ACG	AAT	GTC	TCC	CGG	TTA	AGC	CTA	AAC	CAG	200
Leu	Met	Ala	Val	Leu	Phe	Thr	Asn	Val	Ser	Arg	Leu	Ser	Leu	Asn	Gln	
		40					45					50				

CTC Leu	TGT Cys 55	CTC Leu	GAT Asp	CTC Leu	TCT Ser	CTC Leu 60	CAG Gln	CTC Leu	CAG Gln	TTC Phe	AAT Asn 65	CTC Leu	GTC Val	GGA Gly	TTC Phe	248
ATC Ile 70	TTC Phe	TTC Phe	ATT Ile	ACC Thr	GCC Ala 75	TCC Ser	ATT Ile	TTC Phe	GGA Gly	TTC Phe 80	ACA Thr	GTT Val	ATC Ile	TTC Phe	ATG Met 85	296
TCC Ser	CGA Arg	CCT Pro	AGA Arg	TCC Ser 90	GTT Val	TAC Tyr	CTC Leu	CTC Leu	GAC Asp 95	TAC Tyr	TCA Ser	TGT Cys	TAC Tyr	CTC Leu 100	CCG Pro	344
NCG Xxx	GCG Ala	AAT Asn	CTC Leu 105	AAA Lys	GTT Val	AGC Ser	TAC Tyr	CAG Gln 110	ACA Thr	TTC Phe	ATG Met	AAT Asn	CAT His 115	TCT Ser	AAA Lys	392
CTG Leu	ATT Ile	GAA Glu 120	GAT Asp	TTC Phe	GAC Asp	GAG Glu	TCG Ser 125	TCG Ser	CTT Leu	GAG Glu	TTC Phe	CAG Gln 130	CGG Arg	AAG Lys	ATC Ile	440
CTG Leu	AAG Lys 135	CGA Arg	TCC Ser	GGT Gly	CTC Leu	GGC Gly 140	GAA Glu	GAG Glu	ACT Thr	TAC Tyr	CTC Leu 145	CCG Pro	GAA Glu	TCT Ser	ATC Ile	488
CAC His 150	TGC Cys	ATC Ile	CCG Pro	CCG Pro	CGT Arg 155	CCG Pro	ACT Thr	ATG Met	GCG Ala	GCG Ala 160	GCG Ala	CGT Arg	GAG Glu	GAA Glu	TCG Ser 165	536
GAG Glu	CAG Gln	GTA Val	ATC Ile	TTC Phe 170	GGT Gly	GCA Ala	CTC Leu	GAC Asp	AAT Asn 175	CTC Leu	TTC Phe	GAG Glu	AAT Asn	ACC Thr 180	AAA Lys	584
ATC Ile	GAC Asp	CCT Pro	AGG Arg 185	GAG Glu	ATT Ile	GGT Gly	GTT Val	GTG Val 190	GTG Val	GTG Val	AAC Asn	TGC Cys	AGC Ser 195	TTG Leu	TTT Phe	632
AAC Asn	CCG Pro	ACG Thr 200	CCT Pro	TCT Ser	TTA Leu	TCC Ser	GCC Ala 205	ATG Met	ATT Ile	GTG Val	AAC Asn	AAG Lys 210	TAT Tyr	AAG Lys	CTT Leu	680
AGA Arg	GGA Gly 215	AAC Asn	GTG Val	AAG Lys	AGC Ser	TTT Phe 220	AAC Asn	CTC Leu	GGA Gly	GGA Gly	ATG Met 225	GGA Gly	TGT Cys	AGG Arg	GCT Ala	728

GGT Gly 230	GTC Val	ATC Ile	GCC Ala	GTT Val	GAT Asp 235	CTC Leu	GCT Ala	AAT Asn	GAC Asp	ATT Ile 240	TTA Leu	CAG Gln	CTC Leu	CAT His	AGA Arg 245	776
AAC Asn	ACA Thr	TTA Leu	GCT Ala	CTT Leu 250	GTG Val	GTT Val	AGC Ser	ACA Thr	GAG Glu 255	AAC Asn	ATC Ile	ACT Thr	CAG Gln	AAT Asn 260	TGG Trp	824
TAC Tyr	TTT Phe	GGT Gly	AAC Asn 265	AAC Asn	AAA Lys	GCA Ala	ATG Met	TTG Leu 270	ATT Ile	CCT Pro	AAT Asn	TGC Cys	TTG Leu 275	TTT Phe	AGG Arg	872
GTT Val	GGT Gly	GGA Gly 280	TCC Ser	GCG Ala	GTT Val	CTG Leu	CTT Leu 285	TCG Ser	AAC Asn	AAG Lys	CCT Pro	CGT Arg 290	GAT Asp	CGA Arg	AAA Lys	920
CGA Arg	TCC Ser 295	AAG Lys	TAT Tyr	AAA Lys	CTT Leu	GTT Val 300	CAC His	ACG Thr	GTA Val	CGG Arg	ACT Thr 305	CAT His	AAA Lys	GGA Gly	TCT Ser	968
GAT Asp 310	GAG Glu	AAA Lys	GCA Ala	TTC Phe	AAC Asn 315	TGT Cys	GTG Val	TAC Tyr	CAA Gln	GAA Glu 320	CAA Gln	GAC Asp	GAG Glu	GAC Asp	TTG Leu 325	1016
AAA Lys	ACC Thr	GGA Gly	GTT Val	TCT Ser 330	TTG Leu	TCT Ser	AAA Lys	GAC Asp	CTA Leu 335	ATG Met	TCT Ser	ATA Ile	GCT Ala	GGA Gly 340	GAA Glu	1064
GCT Ala	CTA Leu	AAG Lys	ACA Thr 345	AAT Asn	ATC Ile	ACC Thr	ACT Thr	TTG Leu 350	GGT Gly	CCT Pro	CTG Leu	GTT Val	CTT Leu 355	CCA Pro	ATA Ile	1112
AGC Ser	GAG Glu	CAG Gln 360	ATT Ile	CTG Leu	TTC Phe	ATT Ile	GCG Ala 365	ACT Thr	TTT Phe	GTT Val	GCA Ala	AAG Lys 370	AGA Arg	TTG Leu	TTC Phe	1160
AGT Ser	GCC Ala 375	AAG Lys	AAG Lys	AAG Lys	AAG Lys	AAG Lys 380	AAG Lys	CCT Pro	TAC Tyr	ATA Ile	CCG Pro 385	GAT Asp	TTC Phe	AAG Lys	CTT Leu	1208
GCC Ala 390	TTT Phe	GAT Asp	CAT His	TTC Phe	TGT Cys 395	ATT Ile	CAC His	GCA Ala	GGA Gly	GGT Gly 400	AGA Arg	GCC Ala	GTG Val	ATC Ile	GAT Asp 405	1256

GAA CTA GAG AAG AGT TTA AAG CTA TTG CCA AAA CAT GTG GAG GCT TCT	1304
Glu Leu Glu Lys Ser Thr Lys Leu Leu Pro Lys His Val Glu Ala Ser	
410 415 420	
AGA ATG ACA TTG CAT AGA TTT GGA AAC ACT TCA TCG AGC TCT ATT TGG	1352
Arg Met Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp	
425 430 435	
TAT GAA TTA GCT TAC ACA GAA GCT AAA GGA AGA ATG AGA AAA GGG AAT	1400
Tyr Glu Leu Ala Tyr Thr Glu Ala Lys Gly Arg Met Arg Lys Gly Asn	
440 445 450	
CGA GTT TGG CAG ATT GCT TTT GGA AGC GGC TTT AAG TGT AAC AGC GCG	1448
Arg Val Trp Gln Ile Ala Phe Gly Ser Gly Phe Lys Cys Asn Ser Ala	
455 460 465	
GTT TGG GTG GCT CTT CGT GAT GTC GAG CCC TCG GTT AAC AAT CCT TGG	1496
Val Trp Val Ala Leu Arg Asp Val Glu Pro Ser Val Asn Asn Pro Trp	
470 475 480 485	
GAA CAT TGC ATC CAT AGA TAT CCG GTT AAG ATC GAT CTC TGATTTTCAGC	1545
Glu His Cys Ile His Arg Tyr Pro Val Lys Ile Asp Leu	
490 495	
TTAACCGGTA AAATTGGTCT GTACATATAT TTACCACTGA GTAAAGACAT CAGTTAATGA	1605
TTTGTTGTTA CTCAATTGGG CTAAGTGTAT TATTATATGT GTTGTATATA ATAAAGGTAG	1665
AACGTAAATT TACTAAGAAA AAAAAAAAAA AAAAAAAAAA	1704

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1664 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CA	ATG	ACG	TCT	GTG	AAC	GTA	AAA	CTC	CTT	TAC	CAT	TAC	GTC	ATA	ACC	47
Met	Thr	Ser	Val	Asn	Val	Lys	Leu	Leu	Tyr	His	Tyr	Val	Ile	Thr		
1				5				10					15			
AAC	TTT	TTC	AAC	CTC	TGT	TTC	TTC	CCA	CTG	ACG	GGG	ATC	CTC	GCC	GGA	95
Asn	Phe	Phe	Asn	Leu	Cys	Phe	Phe	Pro	Leu	Thr	Gly	Ile	Leu	Ala	Gly	
				20				25						30		
AAA	GGC	TCT	CGT	CTT	ACC	ACA	AAC	GAT	CTC	CAC	CAC	TTC	TAT	TCA	TAT	143
Lys	Gly	Ser	Arg	Leu	Thr	Thr	Asn	Asp	Leu	His	His	Phe	Tyr	Ser	Tyr	
			35					40					45			
CTC	CAA	CAC	AAN	CTT	ATA	ACC	TTA	ACC	CTA	CTC	TTT	GGC	TTC	ACC	GTT	191
Leu	Gln	His	Xxx	Leu	Ile	Thr	Leu	Thr	Leu	Leu	Phe	Gly	Phe	Thr	Val	
			50				55					60				
TTT	GGT	TCG	GTT	CTC	TAC	TTC	GTA	ANC	CGA	CCC	AAA	CCG	GTT	TAC	CTC	239
Phe	Gly	Ser	Val	Leu	Tyr	Phe	Val	Xxx	Arg	Pro	Lys	Pro	Val	Tyr	Leu	
	65					70					75					
GTT	GAC	TAC	TCC	TGC	TAC	CTT	CCA	CCA	CAA	CAT	CTT	AGC	GCT	GGT	ATC	287
Val	Asp	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Gln	His	Leu	Ser	Ala	Gly	Ile	
80					85					90					95	
TCT	AAG	ACC	ATG	GAA	ATC	TTT	TAT	CAA	ATA	AGA	AAA	TCT	GAT	CCT	TTA	335
Ser	Lys	Thr	Met	Glu	Ile	Phe	Tyr	Gln	Ile	Arg	Lys	Ser	Asp	Pro	Leu	
				100				105						110		
CGA	AAC	GTG	GCA	TTA	GAT	GAT	TCG	TCT	TCT	CTT	GAT	TTC	TTG	AGA	AAG	383
Arg	Asn	Val	Ala	Leu	Asp	Asp	Ser	Ser	Ser	Leu	Asp	Phe	Leu	Arg	Lys	
			115				120						125			
ATT	CAA	GAG	CGT	TCA	GGT	CTA	GGC	GAT	GAA	ACC	TAC	GGC	CCC	GAG	GGA	431
Ile	Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	Tyr	Gly	Pro	Glu	Gly	
		130				135						140				
CTG	TTT	GAG	ATT	CCT	CCG	AGG	AAG	AAT	TTA	GCG	TCG	GCG	CGT	GAA	GAG	479
Leu	Phe	Glu	Ile	Pro	Pro	Arg	Lys	Asn	Leu	Ala	Ser	Ala	Arg	Glu	Glu	
	145					150					155					

ACG Thr 160	GAG Glu	CAA Gln	GTA Val	ATC Ile	AAC Asn 165	GGT Gly	GCG Ala	CTA Leu	AAA Lys 170	AAT Asn 170	CTA Leu	TTC Phe	GAG Glu	AAC Asn 175	AAC Asn 175	527
AAA Lys	GTT Val	AAC Asn	CCT Pro	AAA Lys 180	GAG Glu	ATT Ile	GGT Gly	ATA Ile	CTT Leu 185	GTG Val	GTG Val	AAC Asn	TCA Ser	AGC Ser 190	ATG Met	575
TTT Phe	AAT Asn	CCG Pro	ACT Thr 195	CCT Pro	TCG Ser	TTA Leu	TCC Ser	GCG Ala 200	ATG Met	GTA Val	GTT Val	AAT Asn	ACT Thr 205	TCC Ser	AAG Lys	623
CTC Leu	CGA Arg	AGC Ser 210	AAC Asn	ATC Ile	AAA Lys	AGC Ser	TTT Phe 215	AAT Asn	CTT Leu	GGA Gly	GGA Gly	ATG Met 220	GGT Gly	TGC Cys	AGT Ser	671
GCT Ala 225	GGT Gly	GTT Val	ATC Ile	GCC Ala	ATT Ile	GAT Asp 230	CTA Leu	GCT Ala	AAA Lys	GAC Asp	TTG Leu 235	TTG Leu	CAT His	GTT Val	CAT His	719
AAA Lys 240	AAC Asn	ACA Thr	TAT Tyr	GCT Ala	CTT Leu 245	GTG Val	GTG Val	AGC Ser	ACA Thr	GAG Glu 250	AAC Asn	ATC Ile	ACT Thr	CAA Gln	AAC Asn 255	767
ATT Ile	TAT Tyr	ACC Thr	GGT Gly 260	GAT Asp 260	AAC Asn	AGA Arg	TCC Ser	ATG Met	ATG Met 265	GTT Val	TCG Ser	AAT Asn	TGC Cys	TTG Leu 270	TTC Phe	815
CGT Arg	GTC Val	GGT Gly	GGG Gly 275	GCA Ala	GCG Ala	ATT Ile	CTG Leu	CTC Leu 280	TCC Ser	AAC Asn	AAG Lys	CCG Pro	GGG Gly 285	GAT Asp	CGA Arg	863
AGA Arg	CGG Arg	TCC Ser 290	AAG Lys	TAC Tyr	AAG Lys	CTA Leu	GCT Ala 295	CAC His	ACG Thr	GTT Val	CGA Arg	ACG Thr 300	CAT His	ACC Thr	GGA Gly	911
GCT Ala	GAC Asp 305	GAC Asp	AAG Lys	TCT Ser	TTT Phe	GGA Gly 310	TGT Cys	GTG Val	CGG Arg	CAA Gln	GAA Glu 315	GAA Glu	GAT Asp	GAT Asp	AGC Ser	949
GGT Gly 320	AAA Lys	ACC Thr	GGA Gly	GTT Val	AGT Ser 325	TTG Leu	TCA Ser	AAA Lys	GAC Asp	ATA Ile 330	ACC Thr	GTT Val	GTT Val	GCC Ala	GGG Gly 335	1007

ATA	ACG	GTT	CAG	AAA	AAC	ATA	ACA	ACA	TTG	GGT	CCG	TTG	GTT	CTT	CCT	1055
Ile	Thr	Val	Gln	Lys	Asn	Ile	Thr	Thr	Leu	Gly	Pro	Leu	Val	Leu	Pro	
				340					345					350		
CTG	AGC	GAA	AAA	ATC	CTT	TTT	GTC	GTT	ACA	TTC	GTA	GCC	AAG	AAA	CTA	1103
Leu	Ser	Glu	Lys	Ile	Leu	Phe	Val	Val	Thr	Phe	Val	Ala	Lys	Lys	Leu	
			355					360					365			
TTA	AAA	GAT	AAG	ATC	AAA	CAC	TAT	TAC	GTG	CCG	GAT	TTC	AAA	CTT	GCA	1151
Leu	Lys	Asp	Lys	Ile	Lys	His	Tyr	Tyr	Val	Pro	Asp	Phe	Lys	Leu	Ala	
		370					375					380				
GTA	GAT	CAT	TTC	TGT	ATT	CAT	GCG	GGA	GGT	AGA	GCC	GTG	ATA	GAT	GTG	1199
Val	Asp	His	Phe	Cys	Ile	His	Ala	Gly	Gly	Arg	Ala	Val	Ile	Asp	Val	
	385					390					395					
TTA	GAG	AAG	AAC	TTA	GGG	CTA	TCG	CCG	ATA	GAT	GTG	GAG	GCA	TCA	AGA	1247
Leu	Glu	Lys	Asn	Leu	Gly	Leu	Ser	Pro	Ile	Asp	Val	Glu	Ala	Ser	Arg	
400					405					410					415	
TCA	ACA	TTA	CAT	AGA	TTT	GGG	AAT	ACA	TCG	TCT	AGT	TCA	ATT	TGG	TAT	1295
Ser	Thr	Leu	His	Arg	Phe	Gly	Asn	Thr	Ser	Ser	Ser	Ser	Ile	Trp	Tyr	
				420					425					430		
GAA	TTA	GCA	TAC	ATA	GAG	CCA	AAA	GGA	AGG	ATG	AAG	AAA	GGT	AAT	AAA	1343
Glu	Leu	Ala	Tyr	Ile	Glu	Pro	Lys	Gly	Arg	Met	Lys	Lys	Gly	Asn	Lys	
			435					440					445			
GCT	TGC	CAA	ATA	GCT	GGT	GGG	TCA	GGT	TTT	AAG	TGT	AAT	AGT	GCG	GTT	1391
Ala	Cys	Gln	Ile	Ala	Gly	Gly	Ser	Gly	Phe	Lys	Cys	Asn	Ser	Ala	Val	
		450					455					460				
TGG	GTC	GCT	TTA	CGC	AAT	GTC	GAG	GCT	TCA	GCT	AAT	AGT	CCT	TGG	GAA	1439
Trp	Val	Ala	Leu	Arg	Asn	Val	Glu	Ala	Ser	Ala	Asn	Ser	Pro	Trp	Glu	
	465					470					475					
CAT	TGC	ATT	CAC	AAA	TAT	CCG	GTT	CAA	ATG	TAT	TCT	GGT	TCA	TCA	AAG	1487
His	Cys	Ile	His	Lys	Tyr	Pro	Val	Gln	Met	Tyr	Ser	Gly	Ser	Ser	Lys	
480					485					490					495	
TCA	GAG	ACT	CCT	GTC	CAA	AAC	GGT	CGG	TCC	TAATTTATGT ATCTCAAATG					1537	
Ser	Glu	Thr	Pro	Val	Gln	Asn	Gly	Arg	Ser							
				500												

ATGTTGTCCA CTTTCTCTTT TTTTTTTTCT TTTTITAGTT ATAATTTAAT GGTACGATG 1597

TTTTGTCTAG GTCGTTATAA ATAAAGAATA CATGGGTGTT ACTAGTATAA AAAAAAAAAA 1657

AAAAAAA 1664

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1732 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CTTTCTTCTT	CCCCAACA	ATG	ACC	CAT	AAC	CAA	AAC	CAA	CCT	CAC	CGG	GCA	51	
		Met	Thr	His	Asn	Gln	Asn	Gln	Pro	His	Arg	Ala		
		1				5					10			
GTT	CCG	GTT	CAC	GTT	ACA	AAC	TCC	GAT	CAA	AAC	CAA	AAC	CAA	99
Val	Pro	Val	His	Val	Thr	Asn	Ser	Asp	Gln	Asn	Gln	Asn	Gln	
		15						20				25		
AAC	AAT	CTC	CCA	AAT	TTT	CTC	TTA	TCT	GTT	CGG	CTC	AAA	TAT	147
Asn	Asn	Leu	Pro	Asn	Phe	Leu	Leu	Ser	Val	Arg	Leu	Lys	Tyr	
		30					35					40		
CTT	GGG	TAC	CAT	TAC	CTA	ATC	TCC	AAC	GGT	CTC	TAC	ATC	CTC	195
Leu	Gly	Tyr	His	Tyr	Leu	Ile	Ser	Asn	Gly	Leu	Tyr	Ile	Leu	
	45					50					55			
CCT	CTC	CTC	GGC	GGC	ACA	ATC	GTA	AAA	CTC	TCT	TCC	TTC	ACA	243
Pro	Leu	Leu	Gly	Gly	Thr	Ile	Val	Lys	Leu	Ser	Ser	Phe	Thr	
60					65					70				
GAA	CTC	TCT	CTC	CTC	TAC	AAC	CAC	CTC	CGT	TTT	CAT	TTC	CTC	291
Glu	Leu	Ser	Leu	Leu	Tyr	Asn	His	Leu	Arg	Phe	His	Phe	Leu	
				80					85				90	

ACA	CTC	GCT	ACC	GGA	CTC	TTA	ATC	TCT	CTC	TCC	ACC	GCC	TAC	TTC	ACC	339
Thr	Leu	Ala	Thr	Gly	Leu	Leu	Ile	Ser	Leu	Ser	Thr	Ala	Tyr	Phe	Thr	
			95					100					105			
ACC	CGT	CCT	CGT	CAT	GTC	TTC	CTC	CTC	GAC	TTC	TCA	TGC	TAC	AAA	CCT	387
Thr	Arg	Pro	Arg	His	Val	Phe	Leu	Leu	Asp	Phe	Ser	Cys	Tyr	Lys	Pro	
		110					115					120				
GAC	CCT	TCC	TTA	ATA	TGC	ACT	CGT	GAA	ACA	TTC	ATG	GAC	CGA	TCT	CAA	435
Asp	Pro	Ser	Leu	Ile	Cys	Thr	Arg	Glu	Thr	Phe	Met	Asp	Arg	Ser	Gln	
	125					130					135					
CGT	GTA	GGT	ATC	TTC	ACA	GAA	GAC	AAC	CTC	GCT	TTT	CAA	CAA	AAG	ATC	483
Arg	Val	Gly	Ile	Phe	Thr	Glu	Asp	Asn	Leu	Ala	Phe	Gln	Gln	Lys	Ile	
140					145					150					155	
CTC	GAA	AGA	TCC	GGT	CTT	GGG	CAG	AAA	ACT	TAC	TTC	CCT	GAA	GCT	CTT	531
Leu	Glu	Arg	Ser	Gly	Leu	Gly	Gln	Lys	Thr	Tyr	Phe	Pro	Glu	Ala	Leu	
				160					165					170		
CTT	CGT	GTT	CCT	CCC	AAT	CCT	TGT	ATG	GAA	GAA	GCG	AGA	AAA	GAA	GCA	579
Leu	Arg	Val	Pro	Pro	Asn	Pro	Cys	Met	Glu	Glu	Ala	Arg	Lys	Glu	Ala	
			175					180					185			
GAG	ACT	GTT	ATG	TTC	GGA	GCT	ATA	GAC	TCT	GTT	CTT	GAG	AAA	ACC	GGT	627
Glu	Thr	Val	Met	Phe	Gly	Ala	Ile	Asp	Ser	Val	Leu	Glu	Lys	Thr	Gly	
		190					195					200				
GTG	AAA	CCT	AAA	GAT	ATC	GGA	ATC	CTT	GTC	GTG	AAT	TGT	AGT	TTG	TTT	675
Val	Lys	Pro	Lys	Asp	Ile	Gly	Ile	Leu	Val	Val	Asn	Cys	Ser	Leu	Phe	
	205					210					215					
AAT	CCG	ACG	CCG	TCA	CTT	TCC	GCC	ATG	ATT	GTG	AAT	AAG	TAT	AAG	CTT	723
Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Ile	Val	Asn	Lys	Tyr	Lys	Leu	
220					225					230					235	
AGA	GGA	AAC	ATT	TTG	AGC	TAT	AAT	CTC	GGT	GGA	ATG	GGT	TGT	AGT	GCT	771
Arg	Gly	Asn	Ile	Leu	Ser	Tyr	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser	Ala	
				240					245				250			
GGA	CTT	ATC	TCC	ATT	GAT	CTC	GCT	AAA	CAG	CTT	CTT	CAG	GTC	CAA	CCA	819
Gly	Leu	Ile	Ser	Ile	Asp	Leu	Ala	Lys	Gln	Leu	Leu	Gln	Val	Gln	Pro	
			255					260					265			

AAC Asn	TCA Ser	TAC Tyr 270	GCA Ala	CTA Leu	GTG Val	GTG Val	AGC Ser 275	ACA Thr	GAG Glu	AAC Asn	ATA Ile	ACC Thr 280	TTA Leu	AAC Asn	TGG Trp	867
TAC Tyr	TTA Leu 285	GGC Gly	AAC Asn	GAC Asp	CGA Arg	TCA Ser 290	ATG Met	CTT Leu	CTC Leu	TCT Ser	AAC Asn 295	TGC Cys	ATC Ile	TTC Phe	CGT Arg	915
ATG Met 300	GGA Gly	GGA Gly	GCC Ala	GCC Ala	GTA Val 305	CTT Leu	CTC Leu	TCA Ser	AAC Asn	CGT Arg 310	TCC Ser	TCC Ser	GAT Asp	CGC Arg	ACC Thr 315	963
CGT Arg	TCA Ser	AAA Lys	TAT Tyr	CAG Gln 320	CTC Leu	ATC Ile	CAC His	CCC Pro	GTC Val 325	CGT Arg	ACC Thr	CAC His	AAA Lys	GGA Gly 330	GCC Ala	1011
AAC Asn	GAC Asp	AAC Asn	GCA Ala 335	TTT Phe	GGC Gly	TGC Cys	GTT Val	TAC Tyr 340	CAA Gln	CGA Arg	GAA Glu	GAC Asp	AAC Asn 345	AAC Asn	GAA Glu	1059
GAA Glu	GAA Glu	ACC Thr 350	GCC Ala	AAA Lys	ATC Ile	GGA Gly	GTC Val 355	TCA Ser	CTC Leu	TCT Ser	AAA Lys	AAC Asn 360	CTA Leu	ATG Met	GCA Ala	1107
ATA Ile 365	GCC Ala	GGA Gly	GAA Glu	GCT Ala	CTC Leu	AAG Lys 370	ACA Thr	AAC Asn	ATA Ile	ACA Thr 375	ACA Thr	CTC Leu	GGA Gly	CCA Pro	CTA Leu	1155
GTC Val 380	TTA Leu	CCA Pro	ATG Met	TCC Ser	GAA Glu 385	CAG Gln	ATT Ile	CTG Leu	TTT Phe	TTC Phe 390	CCA Pro	ACA Thr	CTC Leu	GTG Val	GCT Ala 395	1203
CGA Arg	AAA Lys	ATC Ile	TTC Phe	AAA Lys 400	GTC Val	AAG Lys	AAA Lys	ATA Ile	AAG Lys 405	CCT Pro	TAC Tyr	ATA Ile	CCC Pro	GAT Asp 410	TTC Phe	1251
AAG Lys	CTA Leu	GCT Ala	TTC Phe 415	GAG Glu	CAT His	TTC Phe	TGC Cys	ATC Ile 420	CAT His	GCG Ala	GGA Gly	GGT Gly 425	AGA Arg	GCA Ala	GTG Val	1299
CTT Leu	GAT Asp	GAG Glu 430	ATA Ile	GAG Glu	AAG Lys	AAT Asn	TTG Leu 435	GAT Asp	TTA Leu	TCA Ser	GAG Glu	TGG Trp 440	CAT His	ATG Met	GAA Glu	1347

CCA	TCG	AGG	ATG	ACT	TTA	AAC	CGG	TTT	GGT	AAT	ACT	TCG	AGT	AGC	TCA	1395
Pro	Ser	Arg	Met	Thr	Leu	Asn	Arg	Phe	Gly	Asn	Thr	Ser	Ser	Ser	Ser	
	445					450					455					
CTT	TGG	TAT	GAA	CTT	GCG	TAT	AGT	GAA	GCT	AAA	GGG	AGG	ATT	AAG	AGA	1443
Leu	Trp	Tyr	Glu	Leu	Ala	Tyr	Ser	Glu	Ala	Lys	Gly	Arg	Ile	Lys	Arg	
460					465					470					475	
GGA	GAT	AGG	ACT	TGC	CAA	ATT	GCG	TTT	GGA	TCG	GGA	TTT	AAG	TGT	AAT	1491
Gly	Asp	Arg	Thr	Cys	Gln	Ile	Ala	Phe	Gly	Ser	Gly	Phe	Lys	Cys	Asn	
				480					485					490		
AGT	GCG	GTT	TGG	AAA	GCT	TTG	AGA	ACC	ATT	GAT	CCT	ATT	GAT	GAG	AAG	1539
Ser	Ala	Val	Trp	Lys	Ala	Leu	Arg	Thr	Ile	Asp	Pro	Ile	Asp	Glu	Lys	
			495					500					505			
AAG	AAT	CCA	TGG	AGT	GAT	GAG	ATT	CAT	GAG	TTT	CCA	GTT	TCT	GTT	CCT	1587
Lys	Asn	Pro	Trp	Ser	Asp	Glu	Ile	His	Glu	Phe	Pro	Val	Ser	Val	Pro	
	510						515					520				
AGG	ATC	ACT	CCA	GTT	ACT	TCT	AAC	TAGTGT	TTTTT	TTTTTGGG	TC	CAACTAGGGA				1641
Arg	Ile	Thr	Pro	Val	Thr	Ser	Asn									
	525						530									
TAATATTTGT	TATGGTTT	TG	TTCTTACGTA	CGTACTTTAA	GTGATTTAGT	CTAAAAATAA										1701
ATTGGTTTCA	TAAAAA	AAAAA	AAAAA	AAAAA	A											1732

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 622 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27 :

AAG	CTT	AAA	CTA	GTA	TAC	CAT	TAC	TTG	ATC	TCC	AAC	GCC	ATG	TAT	TTG	48
Lys	Leu	Lys	Leu	Val	Tyr	His	Tyr	Leu	Ile	Ser	Asn	Ala	Met	Tyr	Leu	
1				5				10					15			
TTA	ATG	GTG	CCG	CTT	CTA	GCA	GTA	GCC	TTT	GCT	CAT	CTC	TCC	ACG	TTG	96
Leu	Met	Val	Pro	Leu	Leu	Ala	Val	Ala	Phe	Ala	His	Leu	Ser	Thr	Leu	
			20					25					30			
ACG	ATT	CAA	GAT	CTG	GTT	CAT	CTT	TGG	GAA	CAG	CTT	AAG	TTC	AAT	TTA	144
Thr	Ile	Gln	Asp	Leu	Val	His	Leu	Trp	Glu	Gln	Leu	Lys	Phe	Asn	Leu	
		35					40					45				
CTG	TCA	GTA	ACT	CTC	TGC	TCG	AGC	CTT	ATG	GTG	TTT	TTA	GGG	ACT	CTG	192
Leu	Ser	Val	Thr	Leu	Cys	Ser	Ser	Leu	Met	Val	Phe	Leu	Gly	Thr	Leu	
	50					55					60					
TAT	TTC	ATG	AGC	CGA	CCG	ACG	AAG	ATT	TAC	TTG	GTG	GAT	TTC	TCT	TGT	240
Tyr	Phe	Met	Ser	Arg	Pro	Thr	Lys	Ile	Tyr	Leu	Val	Asp	Phe	Ser	Cys	
65					70					75					80	
TAC	AAG	CCG	GAA	AAA	GAG	CGT	ATA	TGC	ACG	AGA	GAG	ATT	TTC	TAT	GAG	288
Tyr	Lys	Pro	Glu	Lys	Glu	Arg	Ile	Cys	Thr	Arg	Glu	Ile	Phe	Tyr	Glu	
				85				90						95		
AGA	TCG	AAA	CTA	ACT	GGG	AAT	TTT	ACC	GAT	GAT	AAT	TTA	ACT	TTC	CAA	336
Arg	Ser	Lys	Leu	Thr	Gly	Asn	Phe	Thr	Asp	Asp	Asn	Leu	Thr	Phe	Gln	
			100					105					110			
AAG	AAA	ATT	ATC	GAA	AGA	TCT	GGA	TTA	GGT	CAG	AAC	ACG	TAC	TTA	CCT	384
Lys	Lys	Ile	Ile	Glu	Arg	Ser	Gly	Leu	Gly	Gln	Asn	Thr	Tyr	Leu	Pro	
		115					120					125				
GAG	GCC	GTT	CTA	CGG	GTT	CCG	CCC	AAT	CCG	TGT	ATG	GCG	GAG	GCT	AGA	432
Glu	Ala	Val	Leu	Arg	Val	Pro	Pro	Asn	Pro	Cys	Met	Ala	Glu	Ala	Arg	
	130					135					140					
AAG	GAG	GCT	GAG	ATG	GTT	ATG	TTC	GGT	GCG	ATC	GAT	GAA	TTG	TTG	GAG	480
Lys	Glu	Ala	Glu	Met	Val	Met	Phe	Gly	Ala	Ile	Asp	Glu	Leu	Leu	Glu	
145					150					155					160	

AAA	ACC	GGG	GTT	AAA	CCT	AAG	GAT	ATC	GGT	ATT	CTT	GTG	GTG	AAT	TGC	528
Lys	Thr	Gly	Val	Lys	Pro	Lys	Asp	Ile	Gly	Ile	Leu	Val	Val	Asn	Cys	
				165					170					175		

AGC	TTG	TTC	AAT	CCG	ACG	CCG	TCT	CTG	TCC	GCA	ATG	GTG	GTT	AAT	CGG	576
Ser	Leu	Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Arg	
			180					185					190			

TAC	AAG	CTT	AGA	GGG	AAT	ATC	ATA	AGT	TAT	AAC	CTT	GGC	GGG	ATG	G	622
Tyr	Lys	Leu	Arg	Gly	Asn	Ile	Ile	Ser	Tyr	Asn	Leu	Gly	Gly	Met		
		195					200					205				

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 residues

(B) TYPE: amino acids

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28 :

Asn Ile Thr Thr Leu Gly
5

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 residues

(B) TYPE: amino acids

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29 :

Ser Asn Cys Lys Phe Gly
5

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other

- (A) synthetic oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CAUCAUCAUC AUGTCGACAA AATGACGTCC ATTAACGTAA AG

42

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other

- (A) synthetic oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31 :

CUACUACUAC UAGTCGACGG ATCCTATTTG GAAGCTTTGA CATTGTTTAG

50

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 residues
- (B) TYPE: amino acids

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE: Xaa at position 3 = Leu or Gly

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32 :

Lys Leu Xaa Tyr His Tyr
5

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other

(A) synthetic oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33 :

CAUCAUCAUC AUGAATTCAA GCTTAARYTN BKNTAYCAYT A

41

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 residues

(B) TYPE: amino acids

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34 :

Asn Leu Gly Gly Met Gly Cys
5

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other

- (A) synthetic oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35 :

CAUCAUCAUC AUGAATTCAA GCTTAAYYTN GGNGGNATGG G

41

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other

- (A) synthetic oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36 :

CUACUACUAC UAGGATCCGT CGACCCATNC CNCCNARRTT

40

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 residues
- (B) TYPE: amino acids
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37 :

Gly Phe Lys Cys Asn Ser
5

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other

(A) synthetic oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38 :

CUACUACUAC UAGGATCCGT CGACSWRTTR CAYTTRAANC C

41

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other

(A) synthetic oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39 :

CUACUACUAC UASWRTTRCA YTTRAANCC

29